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Pred. No. is the number of results predicted by chance to have a

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## ALIGNMENTS

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Shiren, B., Linton, L., Nusbaum, C., Lander, E., Abraham, H., Allen, N., Anderson, S., Barna, N., Bastien, V., Beda, F., Boguslavkiy, L., Anderson, S., Barna, N., Bastien, V., Beda, F., Boguslavkiy, L., Anderson, S., Brown, A., Burkett, G., Campopiano, A., Castle, A., Choepel, Y., Colangelo, M., Collins, S., Collymore, A., Cooke, P., DeArellano, K., Dewar, K., Diaz, J.S., Dodge, S., Ferreira, P., Fitzhugh, W., Gage, D., Galagan, J., Gardyna, S., Ginde, S., Goyette, M., Graham, L., Grand-Pieirre, N., Hagos, B., Heaford, A., Horton, L., Iliev, I., Johnson, R., Jones, C., Kaml, L., Karatas, A., Lakocque, K., Lamazares, R., Landers, T., Lehoczky, J., Levine, R., Lieu, C., Liu, G., Macdonald, P., Marquis, N., McCarthy, M., McEwan, P., McKernan, K., Meldeim, J., Meneus, L., Mihova, T., Mlenga, V., Morrow, J., Murphy, T., Naylor, J., Norman, C.H., O'Connor, T., Pierre, N., Pisani, C., Pollara, V., Raymon, C., Rieback, M., Riley, R., Rogov, P., Rothman, D., Roy, A., Santos, R., Schauer, S., Severy, P., Sougnez, C., Spencer, B., Stange-Thomann, N., Stojanovic, N., Strauss, N., Subramanian, A., Talamas, J., Tesfaye, S., Theodore, J., AC079200 117978 bp DNA linear PRI 01-MAY-2002 Mono sapiens chromosome 8, clone RP11-1058B24, complete sequence. Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo. 1 (bases 1 to 117978)

Birren, B., Linton, L., Nusbaum, C. and Lander, E. Homo, sapiens chromosome 8, clone RP11-1058B24 AC079200.6 GI:20377011 (bases 1 to 117978) Homo sapiens (human) Homo sapiens Unpublished DEFINITION ACCESSION ORGANISM AUTHORS TITLE JOURNAL RESULT 1 AC079200 KEYWORDS SOURCE REFERENCE REFERENCE AUTHORS

Location/Qualifiers 1. .117978

FEATURES

3. (under b. 11/1/2), Nusbaum, C., Lander, E., Ali, A., Allen, N., Anderson, S., Barna, N., Bastlen, V., Bloom, T., Boguslavkiy, L., Boukhgalter, B., Brown, A., Camarata, J., Campopiano, A., Chang, J., Choepel, Y., Colangelo, M., Collins, S., Collymore, A., Cook, A., Chocke, P., DeArellano, K., Dewar, K., Diaz, J.S., Dodge, S., Gard, S., Goyette, M., Gabam, L., Grand, Pierre, N., Gardyna, S., Golds, S., Goyette, M., Gabam, L., Grand, Pierre, N., Hagos, B., Horton, L., Hulme, W., Iliev, I., Grand, Pierre, N., Landers, T., Lehocaky, J., Levine, N., Lancour, R., Machen, C., Macdonald, P., Major, J., Marquis, N., Matthews, C., Macdonald, P., Major, J., Marquis, N., Matthews, C., Macdonald, P., Major, J., Marquis, N., Matthews, C., Norbu, C., Norman, C.H., O'Connor, T., Naquis, N., Matthews, C., Norbu, C., Norman, C.H., O'Connor, T., O'Donnell, P., Schauer, S., Schupback, R., Severy, P., Spencer, B., Stange-Thomann, N., Stojanovic, N., Strauss, N., Subramanian, A., Tavis, N., Trigillo, J., Vassillev, H., Viel, R., Wo, A., Wilson, B., Wu, X., Wwan, D., Ye, W.J., Young, G., Nichi, H., Wilson, B., Wu, X., Wwan, D., Ye, W.J., Young, G., Sichher, A., Viel, R., When, S., Shaner, A. and Zody, M. Shimitted (71-app. 2010) Whitehand Therith, P. Mither, Forter Submission Direct Submission

Submitted (21-APR-2002) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA

4 (Dasses 1 to 117978)

Birren, B., Linton, L., Nusbaum, C., Lander, E., Ali, A., Allen, N., Boukhaler, B., Enowh, A., Camarata, J., Campopiano, A., Chang, J., Chargoliano, A., Chang, J., Chargoliano, A., Chang, J., Chargoliano, A., Chang, J., Chargoliano, A., Chang, J., Faro, S., Cook, P., DeArellano, K., Dewar, K., Diaz, J.S., Dodge, S., Farreira, P., FitzHugh, W., Gage, D., Galagano, A., Gardyna, S., Ginde, S., Gord, S., Goyette, M., Graham, L., Grand Pierre, N., Gardyna, S., Kamat, A., Karzatas, A., Marchan, C., LaRocque, K., Liandazares, R., Landers, T., Lehocaky, J., Lehocaky, J., Larocque, K., Liandazares, R., Macdonald, P., Major, J., Marquis, N., Matthews, C., McCarthy, M., McBan, P., McKernan, K., Maldrim, J., Menens, L., Mihova, T., Maenga, V., Murphy, T., Naylor, J., Marylor, J., Peterson, K., Phunkhang, P., Pierre, N., Pollara, V., Nordov, C., Norman, C.H., O'Connor, T., O'Donnell, P., O'Neil, D., Oliver, J., Peterson, K., Phunkhang, P., Pierre, N., Pollara, V., Kaymond, C., Retta, R., Rieback, M., Santos, R., Schauer, S., Schupback, R., Seaman, S., Severti, M., Travis, N., Tragilio, J., Vassiliev, H., Viel, R., Vo, A., Wilson, B., Mu, X., Waman, D., Ye, W.J., Young, G., Zainoun, J., Zembek, L., Zimmer, A. and Zody, M.

Direct Submitted (01-MA-2002) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA

All repeats were identified using RepeatMasker:

Smit, A.F.A. & Green, P. (1999)

http://ftp.genome.washington.edu/RM/RepeatMasker.html Tirrell,A., Travers,M., Trigilio,J., Vassiliev,H., Viel,R., Vo,A.,
Milson,B., Wu,X., Wyman,D., Ye,W.J., Young,G., Zainoun,J.,
Zimmer,A. and Zody,M.
Direct Submission Direct Submission Submitted (23-AUG-2000) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA 3 (bases 1 to 117978) Withhem C. Lander E. Ali.A., Allen, N., ------ Genome Center Center: Whitehead Institute/ MIT Center for Genome Research Center code: WIBK
Web site: http://www-seq.wi.mit.edu
Contact: sequence submissions@genome.wi.mit.edu Center project name: L10839 Center clone name: 1058\_B\_24 TITLE JOURNAL TITLE JOURNAL REFERENCE TITLE JOURNAL REFERENCE AUTHORS COMMENT

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ORGANISM

REFERENCE AUTHORS TITLE JOURNAL REFERENCE AUTHORS

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Submitted (31-JUL-2002) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA On Jul 31, 2002 this sequence version replaced gi:21699264.
All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997)
http://ftp.genome.washingcon.edu/RM/RepeatMasker.html
                                                                                                                                                                                                                  Center: Whitehead Institute/ MIT Center for Genome Research
                                                                                                                                                                                                                                                                                 Center code: WIBR
Web site: http://www-seq.wi.mit.edu
Contact: sequence submissions@genome.wi.mit.edu
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(clone lib="RPCI-11 Human Male BAC"
68. .989
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11505. .12283
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ement(187="
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| ement(1075)
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/rpt family="MERSA"

complement (1546. .1591)

/rpt family="MLTU2"

complement (1592. .1655)
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complement(17909. .18160)
/rpt_family="AluSx"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             organism="Homo sapiens'
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1090. .4101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /mol_type="genomic_DNA"
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complement (1860. .2187)
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                                                                                                                                                                                                                                                                                                                                                                                                 Center project name: L5118
Center clone name: 675_P_19
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1357. 1540
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5377. .15741
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9408. 9791
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Submitted (14-FEB-2000) Whitehead Institute/MIT Center for Genome Submitted (14-FEB-2000) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA

Research, 3.0 Charles Street, Cambridge, MA 02141, USA

Barna, N., Bastien, V., Bloom, T., Boguslavkiy, L., Boukhgalter, B., Camarata, J., Chang, J., Chazer, B., Choepel, Y., Collymore, A., Cooke, P., DeArellano, K., Dewar, K., Diaz, J.S., Dodge, S., Faro, S., Ferreira, P., FitzGerald, M., Gage, D., Galagan, J., Gard, S., Graham, L., Grand-Flerre, N., Hagos, B., Horton, L., Hulme, W. Illey, T., Johnson, R., Jones, C., Kamat, A., Karatas, A., Kells, C., Landers, T., Levine, R., Lindblad-Toh, K., Liu, G., MacCarthy, M., Meldrim, J., Mencus, L., Micol, R., Mardon, C., Norman, C., Norman, C., Norman, C., Phunkhang, P., Pierre, N., Raymod, C., Retta, R., Rise, C., Rogov, P., Roman, J., Roy, A., Schauer, S., Schupback, R., Seaman, S., Sewery, P., Spencer, B., Stange-Thomann, N., Stojanovic, N., Talamas, J., Zembek, L., Zimmer, A. and Zody, M. Stojanovic, N., Talamas, J., Zembek, L., Zimmer, A. and Zody, M. Direct Submission
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Direct Summission

Edgeserch, 320 Charles Street, Cambridge, MA 02141, USA

Research, 320 Charles Street, Cambridge, MA 02141, USA

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Birren, B., Nusbaun, C., Lander, E., Ali, A., Allen, N., Anderson, S., Barna, N., Bastien, V., Bloom, T., Boguslavkiy, L., Boukhgalter, B., Camarata, J., Chang, J., Chazaro, B., Choepel, Y., Collymore, A., Cooke, P., DeArellano, K., Dewar, K., Didz, J. S., Dodge, S., Faro, S., Ferreira, P., FitzGerald, M., Gage, D., Galagan, J., Godd, S., Graham, L., Grand-Pierre, N., Hagos, B., Horton, L., Hulme, W., Iliev, I., Johnson, R., Lindblad-Toh, K., Liu, G., Maclean, C., Landers, T., Levine, R., Lindblad-Toh, K., Liu, G., Maclean, C., Macdonald, P., Major, J., Matthews, C., McCarthy, M., Meldrim, J., Meneus, L., Mihova, T., Mlenga, V., Murphy, T., Voronnor, T., O'Connor, T., O'Connor, T., O'Connor, J., Ngylor, J., Ngylor, C., Norman, C., Norman, C., Norman, C., Norman, J., Roy, A., Schauer, S., Schulback, R., Seaman, S., Severy, P., Smith, C., Spencer, B., Stange-Thomann, N., Stojanovic, N., Talamas, J., Tesfaye, S., Theodore, J., Topham, K., Travers, M., Vosasiliev, H., Vola, W., Walle, R., Vola, W., Wallen, B., Wy, M., Wyman, D., Young, G., Zainoun, J., Zembek, L., Zimmer, A. and Zody, M.
                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo. 1 (basea 1 to 167118)
Birren, B., Nusbaum, C. and Lander, E. Homo sapiens chromosome 8, clone RP11-675P19
                                                                                                                                                                                  Unpublished
2 (bases 1 to 167118)
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TITLE JOURNAL

REFERENCE

TITLE JOURNAL

REFERENCE AUTHORS

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Dipublished

Signature, S., Linton, L., Nusbaum, C., Lander, E., Abraham, H., Allen, N., Anderson, S., Baraa, N., Bastlen, V., Beda, F., Boguslavkiy, L., Burkert, G., Campoplano, A., Castle, A., Choepel, Y., Colangelo, M., Collins, S., Collymore, A., Cock, P., DeArellano, K., Daza, J.S., Dodge, S., Ferreira, P., Fitzhugh, W. Gage, D., Galagan, J., Gardyna, S., Ginde, S., Goyette, M., Grand-Pierre, N., Hagos, B., Heaford, A., Horton, L., Illav, I., Johnson, R., Jones, C., Kann, L., Karatas, A., LaRcque, K., Lamazares, R., Landers, T., Lehoczky, J., Levine, R., Lieu, C., Liu, G., Macdonald, P., Marquis, N., McCarthy, M., McWann, P., McKernan, K., Morrow, J., Murphy, T., Naylor, J., Norman, C.H., O'Connor, T., O'Donnell, P., O'Neil, D., Olivar, T., Norman, C.H., O'Lover, T., Pisani, C., Pollara, V., Raymond, C., Rieback, M., Riley, R., Schauers, S., Scherry, P., Sougnez, C., Spencer, B., Standes, T., Taslamas, J., Tesfaye, S., Theodore, J., Tirrell, A., Travers, M., Trigillo, J., Vassillev, H., Viel, R., Vo, A., Sannan, D., Ye, W.J., Young, G., Zainoun, J., Wilson, B., Wu, X., Waman, D., Ye, W.J., Young, G., Zainoun, J., Schanmer, A., and Zody, M., Direct Submission
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Homo sapiens chromosome 8 clone CTD-2240Ll map 8, LOW-PASS SEQUENCE
SAMPLING
CGGCTGCTTGCCTGCTCCATCACAGGAAGGTGCAGCAGAGCCCTTTTCTTCCCCAGGGTTG 359
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 63888)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              420 AAGCTGTTCGGGGACTTCCAGAATAAACCAAACCAGCTGTATTACTGGTCTTTGACATCC
                                                                                                                   360 TGGGCACCTTGAACTATCCTGGCTTGCTAAGAAACTGCCCCAAGTGACGCACTC
                                                                                                                                                                                                                                                                                                                                                             480 TCTCTGGTCAGGGCCAAGTCACTGTCCCTGTCTTGGAGAGGGCTTCTGAG 529
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* sequencing reads that have not been assembled into
* contigs. Runs of N are used to separate the reads
* and the order in which they appear is completely
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Contact: sequence submissions@genome.wi.mit.edu
Contact: Project Information
Center project name: Lil1091
Center clone name: 2240_L_1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 (Dasses 1 to 0,000).
Birren, B., Linton, L., Nusbaum, C. and Lander, E.
Homo sapiens chromosome 8, clone CTD-224011
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Web site: http://www-seq.wi.mit.edu
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HTG; HTGS PHASE0.
Homo sapiens (human)
Homo sapiens
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11 probable transmembrane helices predicted for PF10785c by TMHMM2.0 at as 848-870, 877-896, 901-923, 936-958, 978-1000, 1163-1185, 1200-1222, 1243-1265, 1269-1291, 1304-1326 and 1341-1360"
Submitted (20-SEP-2002) P.falciparum Genome Sequencing Consortium, The Welcome Trust Sanger Institute, Wellcome Trust Genome Campus, Hinxton, Cambridge CB10 13A, UK For more information about this sequence or the Malaria Project, see http://www.aanger.ac.uk/Projects/P_falciparum.
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Sanders,M., Hauser,H., Baker,S., Unwin,L., Mungall,K., Berriman,M.,
Pain,A., Hall,N., Bowman,S., Churcher,C., Quail,M. and Barrell,B.
Direct Submission
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              180 TCGGGTATATTTTGGAAGTTGTAAAATACTACRTGTTCTTCTAAGTCCCACTCCTCTG 239
                                                                                                                                                                             9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               89807 CGGCTGCTTGCCTGCTCCATCACAGGAAGGTGCAGCAGCAGCAGCCCTTTTCTTCCCAGGGTTG
                                                                                                                                                                                                                                                                                                               TCTTTATACTTTTATTTATTCCCAAATTTTTCTTAAGCAAATATTTCTTTGCTAATCAAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAATTATCAAAAGAAAAAAACTGAAAGCAACGCTTGAAAAAAAGGAAAGTTAG-CCCTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    240 TTTTCTTTGAGCAGGAAAGAGAAAGCAGTCACCCTCTCTTCCATGACAACAACCCATGAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             300 CGCTGCTTGCCTGCTCCATCACAGGAAGGTGCAGCAGAGGCCCTTTTCTTCCCAGGGTTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TGGGCACCTTGAACTATCCTGGCTTGCTAGCTAAGAAACTGCCCCAAGTGACGCACACTC
                                                                                                                                                                             1 CATGCTGATGCTGTGGTCGTGGTTTATATATGCTGATTTATGCGTGATTTTGCTTCCT
                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Plasmodium falciparum 3D7
Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
1 (bases 1 to 341050)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Barrell, B.G.
Sequence of Plasmodium falciparum chromosomes 1, 3-9 and 13
Nature 419 (6906), 527-531 (2002)
                                                                                                            ï
                                           Length 63888;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 29927 AAGCTGTTCGGGGACTTCCAGAATAAACCAAACCAGCTGTATTA 29970
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             420 AAGCIGIICGGGGACTICCAGAATAAACCAAACCAGCTGTAITA 463
                                                                                                        Indels
                                       Score 451.6; DB 2;
Pred. No. 1.2e-89;
1; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Plasmodium falciparum 3D7
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AL929357.1 GI:23505059
                                    atch 85.4%; sal Similarity 99.6%; 462; Conservative 1
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                                       Query Match
Best Local (
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PFA929357/c
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VERSION
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SOURCE
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JOURNAL
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AUTHORS
                                                                                                     Matches
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LOCUS

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EYILTINKALIEKNITITERREYKYILMILLDLEFERNYASQRADYALNDKYTKOSILISG
EYILTINKALIEKNITITERREYKYILMILLDLEFERNYASQRADYALNYDDKYTKOSILISG
ERINHPHNILHDIDINNERNALIKULYYYYENILMYDYILHYYDLILBODOOYTILHYYL
LIDI FKHMODNKIKIKILTLIKLIYYYENIDYYICYIRKANEKLITINYKEQNISINDT
DORNIEKLADOKKETNDKHHEDETUDSNGEQIDDMHKQORYNKKKAREKLILTINYKEQNISINDT
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KKEETEKSGGTNOKOVOGAHNYKEQNRQDDNNITNEMNEKIRDILKGKKNSHIPIPN
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KTIKIKKYESPEFSERRANESYNOSHIDALSY
IKRIENRAKLISOUDIIKKWEREKALISONNEKEEDILKGTHKGKNSHIPIPN
NETIKIKKYESPEFSERRANESYNOSHIMNINITISDHAKSYNOSHIMVLSYIDE
LSKHFHKYOTLINHNIIDNYNIMDNILYNNMYEDLYNYNNIYDKNSDIMVLSEENM
NRENKYISNNEOYYNDKIRKANANVKLEBOYKNNMKEPLDKEIIKKNNNITPMILYNYDM
NRENKYISNNEOYYNDKIRKONANVALEBOYKNNMKEPLDKEIIKKNNNITPMILYNYDM
NRENKYISNNEOYYNDKIRKONANVALEBOYKNNMKEPLDKEIIKKNNNITPMILYNYDM
NRENKYISNNEOYYNDKIRKONANVALEBOYKNNMKEPLDKEIIKKNNNITPMILYNYDM
NRENKYISNNOSOIMVLYNYDM
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FESHACKNENVALPQINYNASKGKEFTRNMEKQLCHGINFLKNYLLITFIVGIIDLIV
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THYLHAGFYILLADFLTHFIIYFLKDKTILKYVCELELIPWDEKKKLPVHYAEFND
TLISPNEITNYLQGLFQQDNINEEQLKNFFGTDNYEQIYYVILNNLKNQKQMMNITPM
Gallus gallus thioredoxin txN SWALL:THIO CHICK (SWALL:P08629) (104 aa) fasta scores: E(): 1.6e-05, 28.57% and to Ophiophagus hannah thioredoxin txN SWALL:Q98YX1 (RMEL:AF321769) (105 aa) fasta scores: E(): 1.3e-08, 36.44% id in 107 aa"
                                                                                                                                                                                                                                                          /product="thioredoxin, putative"
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/brotein id="CAD51844.1"
/bratein id="1:31556602"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note="Signal anchor predicted for PF10795w by SignalP 2.0 HMM (Signal peptide probabilty 0.152, signal anchor probability 0.803) with cleavage site probability 0.079
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STEQKANPEKEKSKKUKANNNAKANTFYYSNIYIKCYTHAKSVQKPIYIYTYDKAKUH
YFNEYTNYILKKWKKKSFISFYFKQPVILSEIKEQAGNNAIDVENILQNYRLPFVNLE
NFKLYIDDIVSYKQKNVYHIKINTPYKTFMSYQKDHFPYMSHNNVVKYLCIDFSKI"
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15947. .16143,16443. .16553,16671. .16777,16874. .16928))
/gene="PPIO800c"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /trānslation="mgnkmlltkkdknglkkavyiflililipydqwspplvyspcin
krspvlnsigkndngpkyrirdngktilleigwsikeqnvskalanldelflaapddkk
lskkmsmicgnvlnlcgrfndinnmikviekmknhniemqensylaicnyyisnnyiy
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15947. .16143,16443. .16553,16671. .16777,16874. .16928))
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       between residues 40 and 41
1 probable transmembrane helix predicted for PF10795w by TMHMM2.0 at aa 21-43"
/codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                note="No Pfam hit, SMART hit to SM00184, Ring finger"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note="4 probable transmembrane helices predicted for PF10800c by TMHMM2.0 at aa 7-29, 88-110, 130-152 and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NEWVLVHTVEGANQNDIEKĀFQKYCLEKĀK"
join(10913. .11086,11363. .14623)
/gene="PFI0795w"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            join(10913. .11086,11363. .14623)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 join(18553. .20050,20090. .26112)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /product="hypothetical protein"
/protein_id="CAD51845.1"
/db_xref="G1:23505063"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /codon_start=1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /product="hypothetical protein"
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                                                                                                                                                                                                                              codon start=1
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118071 İTATTITATTATTATTATATATÇIRATTATTATTATTATTATTATTATTATTAT
                                                                                                                      Plasmodium falciparum 3D7

Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.

1 (bases I to 22151)

Gardner, M.J., Hall, N., Fung, E., White, O., Berriman, M., Hyman, R.W., Carlton, J.M., Pain, A., Rutherford, K.E., Bowman, S., Paulsen, I.T., James, K., Eisen, J.A., Rutherford, K., Salzberg, S.L., Cralg, A., Kypioli, S., Pertea, M., Allen, J., Selengut, J., Haft, D., Mather, M.W., Vaidya, A.B., Martin, D.M., Fairlamb, A.H., Fraunholz, M.J., Roos, D.S., Ralph, S.A., McRadden, G.I., Cummings, L.M., Subramanian, G.M., Mungall, C., Venter, J.C., Carucci, D.J., Hoffman, S.L., Newbold, C., Davis, R.W., Fraser, C.M. and Barrell, B.
/translation="mtkiondimlpPfSvSSKHCKNNTNvVTYCRTRKRRKRKRKK
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NIDYNNDREIDRLSVDFTYNKLNKKKKKMYDMNKKDNIINVIISDEIMKYNIKNLTT
FCINPYYNNNNNNNNICVLTYKKTVSLIYIYEYHINSVLLFKDDNILNIYMYESFIF
                                                                                                                                                                                                                                                                                                                                                                 AE014844 251551 bp DNA linear INV 11-FEB-2003
Plasmodium falciparum 3D7 chromosome 12, section 1 of 9 of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Genome sequence of the human malaria parasite Plasmodium falciparum
Nature 419 (6906), 498-511 (2002)
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Hyman,R.W. Fung,E., Conway,A., Kurdi,O., Mao,J., Miranda,M.,
Nakao,B., Rowley,D., Tamaki,T., Wang,F. and Davis,R.W.
Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Hyman, R.W., Fung, E., Conway, A., Kurdi, O., Mao, J., Miranda, M.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 3; Length 341050;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 11.0%; Score 58.4; DB 3
Best Local Similarity 57.8%; Pred. No. 0.0098;
Matches 104; Conservative 0; Mismatches 7
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Plasmodium falciparum 3D7
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AE014844 AE014188
AE014844.1 GI:234
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ELHGDLSKATYKKDKNPEGTTPPNPCKLEYQYHTNVTKGEDKGYPCLGRKTVRPSDKE
GAECYKTKI KDSTTDTVGACAPYRRLYMCDRNLEHI EPTKI TTHNLLLDVCLAAQYEG
QSI SQNHGKHQLSYPDSPSQLCTELARSFADIGDI VRGRDLYRGNNRENDKLEKKLKG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LSKETACESQPYDEPRTISINPKNYKNPDIPSHTEYCQACPWCGMTCTFDGKCTKNPE
BELCHHKIVQKEYPDTNYTDIPILPPTTKGNIVBKYRNPCKNSDDNNSDQINNWQCHY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       product="erythrocyte membrane protein 1 (PfEMP1)"
protein id="aaN36090.1"
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Nakao, B., Rowley, D., Tamaki, T., Wang, F. and Davis, R.W.
Direct Submission
Submitted (29-JAN-2003) Stanford Genome Technology Center, Stanford
University, 855 California Avenue, Palo Alto, CA 94304, USA
Location/Qualifiers
                                                                                   1. .251551

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AC117072 146570 bp DNA linear INV 12-MAR-2003 Dictyostelium discoideum chromosome 2 map 3323568-3470138 strain Eukaryota; Mycetozoa; Dictyosteliida; Dictyostelium.

1 (bases 1 to 146570)

Gloeckner, G., Eichinger, L., Szafranski, K., Pachebat, J., Dear, P.,
Lehmann, R., Baumgart, C., Parra, G., April, J.F., Guigo, R., Kumpf, K.,
Tunggal, B., Cox, E., Quail, M.A., Platzer, M., Rosenthal, A. and Dictyostelium discoideum Dictyostelium discoideum AX4, complete sequence. AC117072 AC116964 AC117072.2 GI:28830117 RESULT 6 AC117072/c LOCUS DEFINITION SOURCE ORGANISM ACCESSION VERSION KEYWORDS REFERENCE AUTHORS

TITLE

Sequence and analysis of chromosome 2 of Dictyostelium discoideum Nature 418 (6893), 79-85 (2002) The Dictyostelium Genome Sequencing Consortium 2 (bases 1 to 146570) Baumgart, C. Direct Submission JOURNAL MEDLINE PUBMED REMARK REFERENCE AUTHORS TITLE JOURNAL

Submitted (06-APR-2002) Genome Analysis, Institute of Molecular Biotechnology, Beutenberstr. 11, Jena 07745, Germany 3 (bases 1 to 146570) Submitted (04-MAR-2003) Genome Analysis, Institute of Molecular Biotechnology, Beutenberstr. 11, Jena 07745, Germany 4 (bases 1 to 146570) Direct Submission Baumgart, C. REFERENCE AUTHORS JOURNAL REFERENCE

TITLE

Baumgart, C.

AUTHORS

Submitted (12-MAR-2003) Genome Analysis, Institute of Molecular Biotechnology, Beutenberstr. 11, Jena 07745, Germany On or before Mar 4, 2003 this sequence version replaced gi:19920063, gi:20066239.
CDS predictions from GeneID do not necessarily reflect true gene Further Information is available from IMB Jena, Department of Genome Analysis Direct Submission TITLE JOURNAL COMMENT

(http://genome.imb-jena.de/dictyostellum/)
and the Univerity Colonge, Institute for Biochemistry I
(http://www.uni-koeln.de/dictyostellum/project.shtml
Funding

Agency

FEATURES

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Draft entry and computer-readable sequence [1] kindly submitted by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        82
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1 (bases 1 to 958)
Giorda,R., Ohmachi,T. and Ennis,H.L.
Giorda,R., Ohmachi,T. and Ennis,H.L.
Dictyostellum discoideum spore germination
J. Mol. Biol. 205 (1), 63-69 (1989)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        26 ATTTATATGCTGATTTATGGGTGATTTTGCTTCCTTCTTTATACTTTATTATTCCCAA
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    . 958
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53.0%; Pred. No. 0.49;
vative 1; Mismatches
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/note="109 gene 2 protein"
/codon_start=1
complement (15517. .15972)
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IKALISLIKSSRAMYDLSGKQVIVOLITSIGFVGPINTSPQPQPPPGPPGL
FORELQPHSFLEDDLGTTWELDNLGEN"
join(13881. 13926,14100. 14230,14342. 14589,14703. 15129)
fnote="Genell exon scores (in order of location ranges):
6.11, 2.00, 17.53, 44.25 - GSCJ_ID dd_02599"
/codon_start=1
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PQLANNIKDEMQKIKNQVNLSGLIKNKKEFLDSFKESKLSPTVQRLCELIINYKMY
PSEKYYLCAVEKMLNVSTLPHLTPEEVIEFNKNQNSGSRLNSSTNTTTTTTTTTTTT
PTEKKUNNDQPNLDSFAFSSSFTTSFPSDTTSSTSTSLSTDGEMKDLDVEQQKDDTDNT
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translation="MTILASISSIGNVKSISKSNNVSLSNSSSSLQSMNSIQCGCCGN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NGGLLGANGGLVGGVITGTGYINGSYLHGGGSNINGGGN"
join(7061. 7150,727. 8279,8516. 9178)
/note="GeneID exon scores (in order of location ranges):
-0.28, 67.69, 40.02 - GSCJ_ID dd_03341"
/codon_start=1
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/protein id="AAO52597.1"
/db_xref="G1:28830124"
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join(6487. .649).6572. .86825
/notes="Genello exon scores (in order of location ranges):
3.30, 26.87 - GSCJ_ID dd_03141"
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/note="GeneID exon scores (in order of location ranges):
18.88, 1.20 - GSCJ_ID dd_02598"
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'protein id="AAM33150.2"
'db_xref="G1:28830126"
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protein id="AAO52599.1"
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(http://genome.imb-jena.de/dictyostellum/)
and the Univerity Colonge, Institute for Biochemistry
(http://www.uni-koeln.de/dictyostellum/project.shtml
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Dictyostelium discoideum
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AC116988
<178. .805
/gene="TUBA"
806. .916
/gene="TUBA"
917. .>1662
/gene="TUBA"
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llarity 53.3%;
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                /db_xref="G1:167574"
/translation="MNIRNS:LILISTILFFSIINGS:LSLDPTCVGAPDGQVYLFSSW
DFKGDRXVXNVSQGYLS:LSDGFRGNVQSFISGADVCFVKWYPIEQYQITAGESHRNYA
ALTHFQQRMDAIIPGNCSPK"
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CKNSLDIEKPYTHJARLIAQVISSJTSSLRFPGQLALDINDIQNEVPSPRLDNEAITN
ICKNSLDIEKPYTHJARLIAQVISSJTSSLRFPGQLALDINDIQNEVPSPRLHFVL
CSYAPVISREKAPHETITVDNITSAVFSEKNIMAKCQPNLGKYMACCLMYRGDIVPKE
AGKAVQNIRSEKSRNVSFVDNSPTGFKCGINNQAPVSTKDSBNAEVKKSVCMLSNTTA
ISQVFSRINHKFDLMFVKRAFVHWYVGEGMEEGEFAEARDDLLALEKDYESVSASTEG
EEQEEEY"
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complete cds.
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SDVNNLAKDLGTFFSESTNGKKVVPRAIFLDLEPTVIDEIRTGDYKNLFHPEQLITGK
EDAANNYARGHYTVGKELIDVCVDRIRRLADQCDGLQGFLVFHSVGGGTGSGFGSLLL
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The highly divergent alpha- and beta-tubulins from Dictyostelium discoideum are encoded by single genes
J. Cell. Sci. 105 (Pt 4), 903-911 (1993)
                                                                                                                                                                                                                                                   164 TTTTATTTATGATGATATTAAATATATATAAAATGTACATTTACCAACTGAAATTAAG
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. Clontech) DNA.
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alpha-tubulin.
Dictyostelium discoideum
Dictyostelium discoideum
Eukaryota: Mycetozoa; Dictyosteliida; Dictyostelium.
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tubulin (TUBA) gene,
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/gene="TUBA"
join(178. .805,917. .1662)
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/protein_id="AAC37343.1"
/db_xref="G1:290059"
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/tissue_lib="Clontech"
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                                                                                                                                              53.3%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                284 raararrGarrrrr 298
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     gene="TUBA"
                                                                                                                                                            Best Local Similarity 53.3
Matches 104; Conservative
                                                                                                          Unreported.
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(library:
                                                                                                                                                                                                                                                                                      107
                                                                                                                                              Query Match
                                                                                                                                                                                                                                                                                                                                                          167
                                                                                      BASE COUNT
ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DEFINITION
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VERSION
KEYWORDS
SOURCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PUBMED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 8
DDITUBA
LOCUS
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                                                                                                                                                                                                                                                                                                2121 TTTTATTTATGATGATATTAATTAAATATAAAATGTACATTTACCAACTGAAATTAAG 2180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2181 AAAGTCGGTTAATAAACTTGGATTTTTTTTTTTTAAGTTTTTTTAATTATCCAAAGTAAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AC116988 331039 bp DNA linear INV 12-MAR-2003
Dictyostelium discoideum chromosome 2 map 6445720-6776760 strain
                                                                                                                                                                                                                                                                                                                                                                      107 CTTTGCTAATCAATAAATTATCAAAAGAAAAAAAAACTGAAAGCAACGCTTGAAAAAAGG 166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         167 AAAGTTAGCCCTATCGGGTATATTTTGGAAGTTGTAAAATACTACRTGTTCTTCTAAG 226
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Submitted (12-MAR-2003) Genome Analysis, Institute of Molecular Biotechnology, Beutenberstr. 11, Jena 07745, Germany Om Mar 4, 2003 this sequence version replaced gi:20042960. CDS predictions from GeneID do not necessarily reflect true genes. Further Information is available from IMB Jena, Department of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Mycetozoa; Dictyosteliida; Dictyostelium.

1 (bases 1 to 331039)
Glockner, G., Eichinger, L., Szafranski, K., Pachebat, J., Dear, P.,
Lehmann, R., Baumgart, C., Parra, G., April, J. F., Guigo, R., Kumpf, K.,
Tunggal, B., Cox, E., Quail, M.A., Platzer, M., Rosenthal, A. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence and analysis of chromosome 2 of Dictyostelium discoideum Nature 418 (6893), 79-85 (2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Molecular
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Submitted (04-MAR-2003) Genome Analysis, Institute of Molecular
Biotechnology, Beutenberstr. 11, Jena 07745, Germany
4 (Dases 1 to 31039)
                                                                                                                                                                                                                                    47 IGATITICCTICCTICTTATACTTTTATTTCCCAAATTTTTCTTAAGCAAATATT
                                                                                                                                                                 Gaps
                                                                                                                                                                 .
                                                                                              Length 2255;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Biotechnology, Beutenberstr. 11, Jena 07745, Germany 1 (bases 1 to 331039)
                                                                                                                                                                 Indels
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                                                                                                                                                              90;
                                                                                              DB 3;
                                                                                           Score 50.6; DB Pred. No. 0.65; 1; Mismatches
825
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source

CDS

CDS

FEATURES

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DATKKILSNEGLVAFYHGIIPAYFKVVPTVAISFAVYEICKDLGSNKYQQK"
join(20299. .20406,20551. .20660,20960. .21569,21708. .21828,
22984. .24188)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             .27884)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              complement (join(13231. .14884,15364. .15368))
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IIRLLIEMNDIINYKDIRIYLPNQSEERKLLMKIREGEEIDIQSCFELVQSKYLEFEE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LKDSKEFYFGDIVLFGDQTLNPNILDTNILTFITNFTSMEPEKKKVSDQLITAKNLLD
QSPSCSCLVSRNGKIIRKIGAFYERLLGLEIGENISSVBKSSDISTILKQVOFBNNL
STETTITKRGGEKYPAEVFYKEISDIHSNSTGIMIIVRDITODIRLKEMNIELQKKSE
LEGKRNQELMEBALDLALTAKIKSGPISHSIRTPLNGIITMGEMLSTSPLNTEG
HDIAFTIFGSSBLLLSITSDILDFSKIEASKLELEMIEFDFTGCLEGIGKTIGVSITH
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RKYGFPAEYAVFPIGCLVKNNELSSOKEIAANWISFPTAYYGLVBFAQIKKGDYVIIT
                                                                                                                                                                                                                                                                                                                                                                                                           AGSAGTSLAGIAIAKEFGAHTIVTSNBEKKKOOILDYGADYFVSLDTBDIVKRTFEIT
NGKGANIIYDSVGGQSAQKLFESSSQFGKIVPYGNMNHSEPTPLPILIGLKNYLTIKV
LNTNEYLYQPEPNKKAIEFLNSNFHHFKSIVGKEFIGIDSLVDALKYLETGDLFGKVV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CGSGSEMKYTVPQTWFSGAMAGLTSTFFTYPLDVVRIRLSLQGSCSNDYAAHRYNGIT
HSFFKIHKDEGVKGLYKGLGTSIASIVPWVSISFATYEGFKIICKKMILNYQISSSSL
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                  /translation="wtilksissmgisnrknsfspvstnsmietnonvnsvsksgysk
Likgaalmaegisgpp"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  VASDENBLKKGVNMICDFVCGALSGAVTMTVCYPLDVLRRRMMIQGIGGNKVLYKNGW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /trānslation="MILKFIIQOCVFKVAKIFSDNLIQIFMDISSVYSSSTLFPSKLS
LLMCKVFNSKCAGISVLNKDGLFDTIAFCSSTQELENFSYSLKKISKNITYYDYMEIP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /codon_gtart=1
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/note="GeneID exon scores (in order of location ranges):
-2.62, 6.90, 11.20, 259.32 - GSCJ_ID dd_01978"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note="GeneID exon scores (in order of location ranges): 9.06, -2.15, 55.50, 6.70, 58.02 - GSCJ_ID dd_01980"
                                                                                      complement (11515. .12534)
                                                                                                                                                                                                                                       oxidoreductase"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /pseudo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "KVNN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CDS
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                                                                                      CDS
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98.40, 31.82 - GSCJ_ID dd_02784"
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KFYAPWCGHCKKLAPDFELILATINHAKTNVKVARANSNVDLSPSNFDSVVLDKS
KIPDKSTTAKDYNGARSVPBELITYINHAKTNVKVKARANSNVDLSPSNFDSVVLDKS
KRVLVEFYAPWCGHCKKLMPDFELIGNTYANEKDVVIAKIDCDAADNKALCSKYGVTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LKGNGGKDATQEFDDVGHSASAĪAKMOSLRICRIEGAKPREEKKKEIKKTTTTSAPK
QQESAGLGLLKIPLIIIVLAIAAYFFWGDQQ"
complement(join(2345. ,3098,3189. ,3526))
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PPILKWFGKQSKDGEKYEGGRDLDTFINYINKQAGWNRVKGGKLAVGAGRVEGLDTIA
TEFIAAAAEVRKELVKKAQTVVDSLPEELRTEGSYYVKVMKTIAEKSIDFVTTEIARI
YKLVSGSMSGKKADEPAKKLNILESFKSK"
join (5795. . 6179, 6292. . 6567, 6659. . 6881, 7332. . 7363,
7523. . 8215, 8284. .10451)
/note="GeneID exon scores (in order of location ranges):
14.11, 5.65, 10.80, 0.73, 45.28, 141.12 - GSCJ_ID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /db_xxef="G1:28829384"
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SDREFCDFSFEILCYNBAMDEODQLMFTDFPYSEMIRSDFGSIG1THTALSFGS
SDREFCDFSFEILCYNBAMDEODQLMFTDFPYSEMIRSDFGSIG1G1THTALSFGS
LKYPLNNLYINFGTYDLNIYYSCEMIDYELMKVKILKPNYFKKNLYGNGIIQLIG
LKYPLNNLYIRGGSAPPLNFNYFLISLEELDGGTVENYNISLLEYGFFTIVTFPAT
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complement(join(912. .1165,1280. .1427))

/note="GeneID exon scores (in order of location ranges):

30.46, 12.19 - GSCJ_ID dd_02783"

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1.76, 12.26 - GSCJ_ID dd_02786"
'codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NOSKLTTPOLIGIIIGSIAFAAVIAISIAYHIIKKKKDTKFKNGLONKLKTFKS"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /product="similar to Dictyostellum discoideum (Slime mold). Hypothetical 127.0 kDa protein" /protein_id="AAM34336.2"
                        Deutsche Forschungsgemeinschaft (DFG).
Location/Qualifiers
                                                                                                               organism="Dictyostelium discoideum"
mol_type="genomic DNA"
strain="AX4"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                oin(11030. .11042,11114. .11283)
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/protein_id="AAO51923.1"
                                                                                                                                                                                                         db_xref="taxon:44689"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       codon start=1
                                                                                      .331039
Funding
                           Agency
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CDS

SGS

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DNA linear HTG 03-MAY-2003
*** SEQUENCING IN PROGRESS ***, 6
                                                                                                                                                                                                                                                                                                              Submitted (02-MAY-2003) Wellcome Trust Sanger Institute, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries:
zish.help@sanger.ac.uk Clone requestes: clonerequest@sanger.ac.uk On May 3, 2003 this sequence version replaced gi:30142548.
                                                                                                                                                                                           Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Ostariophysi;
Cypriniformes; Cyprinidae; Danio.
1 (bases 1 to 16744)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Assembly program: XGAP4; version 4.5
Chemistry: Dye-terminator; 100% of reads
Chosensus quality: 11041 bases at least Q40
Consensus quality: 12485 bases at least Q30
Consensus quality: 13485 bases at least Q20
Insert size: 16244; sum-of-contigs
Insert size: 173147; 3.5% error; agarose-fp
Quality coverage: 1.49x in Q20 bases; sum-of-contigs Quality
coverage: 0.60x in Q20 bases; agarose-fp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             as soon as it is available and the accession number will be preserved.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    * NOTE: This is a 'working draft' sequence. It currently consists of 6 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        8872: contig of 2246 bp in length 8972: gap of 100 bp 11234: contig of 2262 bp in length 11334: gap of 100 bp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1674: Gap of 100 bp
1674: contig of 2505 bp in length.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  gap of 100 bp
contig of 3262 bp in length
gap of 100 bp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3164: contig of 3164 bp in length 3264: gap of 100 bp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        100 bp _ of 2805 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           note="assembly_fragment:00047"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   note="assembly_fragment:00233"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      5627. 8872
/note="assembly_fragment:00455"
                                                                                                                                                                                                                                                                                                                                                                                                                                                      BX469924 16744 bp
Danio rerio clone CH211-117012,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /mol_type="genomic DNA"
/db_xref="taxon:7955"
/clone="CH211-117012"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         l. .16744
/organism="Danio rerio"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   clone lib="CHORI-211"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          14139: contig of
14239: gap of 10(
16744: contig of
                                                                                                                   BX469924.2 GI:30349857
                                                                                                                               HTG; HTGS PHASE1.
Danio rerio (zebrafish)
Danio rerio
                                                                                                                                                                                                                                                                                                  Direct Submission
                                                                            unordered pieces.
                                                                                                                                                                                                                                                                                                                                                                                                                                       Center code: SC
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3265
6527
6627
8873
8973
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14140
14240
                                                                                                                                                                                                                                                                             Burton, J
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                                     LOCUS
DEFINITION
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KEYWORDS
SOURCE
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AUTHORS
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                  BX469924
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of PPMALBP1 from base 100001 (AL844507 Plasmodium falciparum 3D7
                                                                                                                                                                                                                                                                                                                                                                                              267553 TAATATTGTTTTATATATTTTTTTTTTTTTTCTTGAAAAGATTTTTACTTAAAACAAAT 267494
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LERSKPGVGSLFSVTLNFEQIGSNTLKSLLPDKSFSRNKTCIILDNYEYTASIASQRF
DQIFEESNIILVKESTVKKFFELVQEYKINGDVNKIDLKNLDPELLPFFDSSLICIIV
FHRFMDNLDIFLKYVKDFIEFYKKKIVVALGINHKNFKNLPKRRDFLIFKKPISSTNL
                                                                          IKVSNMARKI I PKSSSSSNLI QTI SQI DNQQQQQQQQQQQQQQQQQQQQQQQQQ
VTI SPHSDSSEKKTTPKKDRGKYDFNI SPLRI DRFGTESTSSPKI KLYSDTSSDSGES
DEFEFSENLRELKSDGELVVLKNQQYKEQRLSNI QLINDPI VTPPTPKANSEVVSTKA
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KIKISIDDSGIGIGEDQRAHLFEPFHQIDSSSTRKYGGSGLGLAISSKLAKLMGGEV)
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                                                                                                                                                                                                                                                                         Score 50.6; DB 3;
Pred. No. 0.52;
0; Mismatches 94;
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55.8%; Pred. No. 0.6;
iive 0; Mismatches 76;
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1310000
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                                                                                                                                                                                                                                                                           Query Match 9.6%;
Best Local Similarity 53.2%;
Matches 107; Conservative
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PRMAL8P1 01
PFMAL8P1 03
PFMAL8P1 03
PFMAL8P1 04
PFMAL8P1 06
PFMAL8P1 06
PFMAL8P1 06
PFMAL8P1 09
PFMAL8P1 09
PFMAL8P1 09
PFMAL8P1 10
PFMAL8P1 12
PFMAL8P1 12
PFMAL8P1 12
PFMAL8P1 11
PFMAL8P1 13
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PFMAL8P1 13
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PFMAL8P1 13
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PFMAL8P1 13
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Best Local Similarity
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Best Local Similarity
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Lardy, B., Klein, G. and Bof, M.
Direct Submission
Submitted (17-JAN-2003) Departement Reponse et Dynamique
Cellulaires (UMRS092 CNRS), CEA-Grenoble, 17 rue des Martyrs, 38054
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GVLYPLLYPLSPLGPLKAIFHQYYVAAALMAGLSVLCYFLVPTWLAAMVMDISAVVPL
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Dictyostelium discoideum p22-like superoxide-generating NADPH
Oxidase light subunit gene, complete cds.
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                                                                                                                                                                                                                                                                                                                       4634 İTİİGTİTÇİTÇAARAİTTACTAAAAGITATİRİTİTAACATATİTACTTACAAATAAAT 4693
                                                                                                                                                                                                                                                                                                                                                                                                 4694 AAATAAATAAATAAATAAATAAATAAATAAATAAATATGGCCACACTTTACAATGT 4753
                                                                                                                                                                                                                                                                                  61 ICTTTATACTTTTATTATTCCCAAATTTTTCTTAAGCAAATATTTCTTTGCTAATCAAT 120
                                                                                                                                                                                                                                                                                                                                                                121 AAATTATCAAAAGAAAAAAAAACTGAAAGCAACGCTTGAAAAAAGGAAAGTTAGCCCTAT 180
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/db_xref="taxon:44689"
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/db_xref="taxon:44689"
/product="p22-11ke superoxide-generating NADPH oxidase
1ight subunit.
/codon_start=1
/product="p22-11ke superoxide-generating NADPH oxidase
/jointl. n22,284. 518)
/codon_start=1
/product="p22-11ke superoxide-generating NADPH oxidase
light subunit.
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                                                                                                                                                                Gaps
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Dictyostellum discoideum
Blatyostellum discoideum
1 (bases 1 to 518)
Lardy, B., Klein, G. and Bof, M.
Dictyostellum discoideum superoxide-generating NADPH oxidases Unpublished
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                                                                                                                                                           2;
                                                                                                                                                                                                                                                                                                                                                                                                                                              181 CGGGTATATTTTGGAAGTTGTAAAATACTACRTGTTCTCTTCTAAGTCC 229
                                                                                                                      Length 16744;
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                                                           534 others
                                                                                                                   Score 49.8; DB 2; Length 1 Pred. No. 0.89; 1; Mismatches 103; Indels
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        14240. .16744
|14240. .16744
|/note="assembly_fragment:00601"
| 2401 c 3068 g 5010 t
/note="assembly_fragment:00571"
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Location/Qualifiers
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Best Local Similarity 55.1%;
Matches 97; Conservative
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AUTHORS
TITLE
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AUTHORS
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KEYWORDS
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79; Indels

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26 ATTTATATGCCTGATTTATGCCTGATTTTGCTTCCTTCTTTATACTTTTATTTTATTCCCAA

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AC116982 256879 bp DNA linear INV 12-MAR-2003 Dictyostelium discoideum chromosome 2 map 3622643-3879522 strain
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of
86 ATTTTTCTTAAGCAAATATTTCTTTGCTAATCAATAAATTATCAAAAGAAAAAAACTG 145
                                                                                                                                                                                                      217 ATTTTTTAAATTAAGTATTTATTAATAATTTTAAATTTTCAAATATAAATATA 158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Mycetozoa; Dictyostellida; Dictyostellum.

[ (bases 1 to 256879)
[ (lockner, G., Eichinger, L., Szafranski, K., Pachebat, J., Dear, P., Lehmann, R., Baumgart, C., Parra, G., April, J.F., Guigo, R., Kumpf, K., Tunggal, B., Cox, E., Quail, M.A., Platzer, M., Rosenthal, A. and
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complement(join(2498. .3048,3100. .4441,5088. .5120))
/note="GeneID exon scores (in order of location ranges):
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Seguence and analysis of chromosome 2 of Dictyostelium discoideum
Nature 418 (6893), 79-85 (2002)
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Submitted (04-MAR-2003) Genome Analysis, Institute of Molecular
Biotechnology, Beutenberstr. 11, Jena 07745, Germany
4 (bases 1 to 256879)
                                                                                                                                                                                                                                                                                                                                                                       157 AATATAAATCTTAATAATAATAAAAATATAATTACATTGAATAGATTGCTATATAT 102
                                                                                                                                                                                                                                                                                             146 AAAGCAACGCTTGAAAAAAGGAAAGTTAGCCCTATCGGGTATATTTTGGAAGTTGT 201
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(http://genome.imb-jena.de/dictyostellum/)
and the Univerity Colonge, Institute for Biochemistry I
(http://www.uni-koeln.de/dictyostelium/project.shtml
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Location/Qualifiers
1. .256879
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/mol_type="genomic DNA"
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/db_xxef="taxon:44689"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AX4, complete sequence.
AC116982 AC116981 AC115574 AC115677
AC116982.2 GI:28828986
HTG.
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Dictyostelium discoideum
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KEYWORDS
SOURCE
ORGANISM
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AUTHORS
TITLE
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AUTHORS
TITLE
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AC116982
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JOURNAL
MEDLINE
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/note="GeneID exon scores (in order of location ranges):
62.84, 35.15, -1.47 - GSCJ_ID dd_03265"
/codon_start=1
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/note="GeneID exon scores (in order of location ranges):
156.00, 19.78, 12.12 - GSCJ_ID dd_01499"
/codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ILTKVLSEFLHKEIREKGGAYGGGSSVDSGVISFYSYRDPNLIKTLDAFDQSIOWSLN
NKITLENIENAQLSIFSDFDSPESPSNKGYGEWMRDITNEMKQTRRNNLLSITKPKLE
EIATKYLFNNQNNYTTVLGSKDNQELNKFTWNNINV"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /translation="MYLHLERNCKGINSLKSI PRHYMLLDGFKEKLSECILPEGVQNL
FLGDIKQDLTIDSIPNSYKAVYLLNGFNQKKTCRNGISTNKLTCGIIPEGVKTLEICD
IKQQLTIDSIPKYVSEIIIQRKIKQTIIPFQIPKNITLKYAD"
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HHHGHKANDIOTESSTRAINLLANNFKONIYAKLIDRIGNDGFTLNESSTRTKUCLQYN
HNNDLVTKEFKKIHDILSKTELDIKKQLTPFENNQLINBTLANSSLANDIELLSFPIIN
NNNNNNNNNNNNNNNNNNNNNNNNNNNNTIIDKINDFIKKKODFKNYSIDGNTFEIII
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INNVALLINSPEREKLEBGILEKKYHRLFLGDIKQELTINSIFSSYKKYYLLDGFNQKLT
AGILPDGVKNLLLGGIKQDLAIDSIPNSKEFYYLLINGFNRKITAGILPEGVEFFLGG
IKQDLTIHSIPSSVKFVYLLDGFNQKLTAGILPEGVNFLSLGDIKLDLTIDSIPKSVN
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ILPEGVENLFLGDIKQELTIDSIPKSVKYVNLLDGFNQKLTAGIIPEGVKILEICDIK
QLTIDSIPKSVCEIIIPMKQKQTIIPPQIPKNITLKYLDN"
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/note="GeneID exon scores (in order of location ranges):
1.81, 0.51 - GSCJ_ID dd_01491"
/codon start=1
/product="similar to Dictyostelium discoideum (Slime mold): CIGB protein (Fragment)"
/protein id="MAA051566.1"
/db_xref="GI:28828991"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  complement (16692. .17381)
/note="GeneID exon scores (in order of location ranges):
27.91 - GSCJ ID dd_03236"
/codon_start=1
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/protein id="AAOS15681"
/db_xref="GI:28828993"
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Best Local Similarity 52.7
Matches 107; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          complement (join(12095. .14181,14265. .15122,15203. .15458))
/note="GeneID exon scores (in order of location ranges):
207.84, 62.69, 6.20 - GSCJ_ID dd_01492"
                                                                                                                                                                                                                                                                                                                                     FLISLSTYSSEPTSIDENSNSNSNSNSNSPEPKONYLKLISKELNNKENFDFDIKRYI
RSNEMLEFCFTNFNEI ILHPKFKNNLTTWVKMDRTDLIETFNOLIKIOLNDKYNIEND
LILPTIINSGESITTPSIPKOKTOLISYAYLIKKLKETRKNWENSNYLDEKLLESLYL
KUNSKINLDYQLECIKLIIEHTTEOYNPLSIMVQTEIHLFNSTENDLFILKASYINKQ
PLYWLFTNHKVPIPSELSLISALYLSNOIDOFLIEFENHLINESYFOLDIIFEIGKN
SDYKLLGKLIDTFNNFETKSQQSLPKTFNEEKKRLLSLCFFKASVOGNIIIFKFLLEN
YDNILPPKNSKLPEESFLETDESFORYVAKAIEKDNHQLFEFFFQNLGYQSILSELEY
                                                                                                                                                                                              /translation="MSDNTEILFWKDSIPPKDVLNIDLEILIGLCIIIINIPFLKNIK
SSSPPILTEINEIKNYSEKOLKKSININEPUDPWLKALIRFYDDSWRFDIDYNP
PRFLKEDEGDSNEINSHANKIYENILTAYQNOPSIPSLEYCNSKLLEKTINDFGTL
PIFETKLYPQILFREPMKSSDVSKSRYISFISKLILKNLLNPIVLVFLLIEYDDIELID
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VSVYIGPNLVLSNVILNHSDPNVTKINQVKNDKDGFSIKLSGIGFTDSMDASIVLPNG
SRRAIKCKLQCIANLESTNKINISNGTGFYLCTSKAIIDQDSIGLKMIPNSKLIEFDV
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QMPSGTGINKDYILNYNSLVLNNQFSYAQPIINFLTISAKKDMITINGNNFGNSEKVI
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/note="GeneID exon scores (in order of location ranges):
185.43, -3.14 - GSCJ_ID dd_01494"
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/product="similar to Homo sapiens (Human). similar to metalloprotese 1 (pitrilysin family)"
/protein_id="AAM44360.2"
/db_xref="GI:28828990"
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/product="similar to Dictyostelium discoideum (Slime
mold). LagC2"
- GSCJ_ID dd_01255"
                                                                       /product="hypothetical protein"
/protein_id="AAM44355.2"
/db_xref="GI:28828987"
       -0.12
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for replication.
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Submitted (24-JAN-1990) Slade M.B., School of Biological Sciences,
Macquarie University, Sydney NSW 2109, Australia
Location/Qualifiers
1. 5852
/organism="Dictyostelium discoideum"
/mol_type="genomy condition"/mol_type="genomy condition
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Identification of the origin of replication of the eukaryote
Dictypatelium discoideum nuclear plasmid Ddp2
Plasmid 24 (3), 208-217 (1990)
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        DB 3; Length 5850;
                                                                                        Indela
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/note="palindromic sequence tgtcatgaca"
1137. 1638
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Motes palindromic sequence tgtcatgaca"
1285. 1294
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2172. .2181
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          132 AGAAAAAAAACTGAAAGCATGAAAAAAGGAAA 169
                                                                                        68;
    9.3%; Score 49.2; DE 57.0%; Pred. No. 1.3; iive 0; Mismatches
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/cell_line="HU2362"
572. .1072
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/note="palindromic
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                                       Similarity 57.0 90; Conservative
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Dictyostelium discoideum plasmid Ddp2 trans-acting factor gene,
complete cds.
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|protein id="AAA3191.1"
|db_xref="G1:167728"
|translation="MDELISWDRFFKFFVILLEEFKGCKRNDVRLSVDYDILSGIYSP
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SKTKLSQLPTFAPDERYNKETNILKVLDQCDELTRTFLNNYKIANKLSTIENYLYNNF
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Location/Qualifiers
                                                                                                                                                                   TTTATACTTTTATTTATTCCCAAATTTTTCTTAAGCAAATATTTCTTTGCTAATCAATAA 122
                                                                                                                                                                                                                                                                                                                                      ATTATCAAAAGAAAAAAAAACTGAAAGCAACGCTTGAAAAAAAGGAAAGTTAGCCCTATCG 182
trans-acting factor.
Dictyostelium discoideum
Dictyostelium discoideum
Dictyostelium discoideum
Bukaryota, Mycetozoa, Dictyosteliida, Dictyostelium.

(Dases 1 to 5850)
Leiting, B., Lindner, I.J. and Noegel, A.A.
The extrachronosomal replication of Dictyostelium plasmid Ddp2
requires a cis-acting element and a plasmid-encoded trans-acting
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COMPLEMENT (5073. 5113)
//note="putative VECTOR sequence Cloning vector DEMBL 8
minus (pEMBLAm) (X04996); putative"
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/note="putative VECTOR sequence Bacteriophage lambda
(J02459); putative"
2372. .5041
/codon start=1
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/mol_type="genomic DNA"
/strain="WS3808"
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/db_xref="SPTEMBL:023913"
/translation="MDELISWDRFKEFVILLEBERGCKRNDVRLSVDYDILSGIYSP
FTVLKEVFRAVARAVAYDESIDLERLESVFPGTSLYSYIFGIFSLKOFLLISKTKSGK
IRVSDVDQAILIFDHFSRISKQVFRKDIIFGYRTFERSISGRAAGVSWFN
LVSKISTYCKNHPLFAENPTYKHVDFISMLSLVHGIIVDSQNEDENNVSAMYSLNPFV
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/gene="REP gene from a recombinant Ddp-2 like plasmid in
Dictyostelium spp"
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/gene="REP gene from a recombinant Ddp-2 like plasmid in
Dictyostelium spp"
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                                                                     'note="essential for plasmid replication"
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'note="palindromic sequence tggcatgaca"
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Best Local Similarity 57.0%; Pred. No. 1.3;
Matches 90; Conservative 0; Mismatches
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synthetic construct
artificial sequences.
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VERSION
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DLEKSI PGAYOSKYTTNRTRGSRSNNLNNPTTTTTTTTTTTTTAPITTRSKRKSDD
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Dictyostelium discoideum chromosome 2 map 5515173-5817331 strain
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 72 TTATTTATTCCCAAATTTTTCTTAAGCAAATATTTCTTTGCTAATCAATAAATTATCAAA 131
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[ (bases 1 to 3021s6)
[ dlockner, G., Eichinger, L., Szafranski, K., Pachebat, J., Dear, P., Lehmann, R., Baumgart, C., Parra, G., April, J.F., Guigo, R., Kumpf, K., Tunggal, B., Cox, E., Quail, M.A., Platzer, M., Rosenthal, A. and
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Nature 418 (6893), 79-85 (2002)
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Best Local Similarity 57.0%; Pred. No. 1.3;
Matches 90; Conservative 0; Mismatches
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Dictyostelium discoideum
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LMDLKVVKPIARQHYQMDLFKFFFSLNQLLVYLRIYLSLFKKDYYFYSKLYFTLEIKI
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Submitted (12-MAR-2003) Genome Analysis, Institute of Molecular Biotechnology, Beutenberstr. 11, Jena 07745, Germany 5 (bases 1 to 302156)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (http://genome.imb-jena.de/dictyostalium/)
and the Univerity Colonge, Institute for Biochemistry
(http://www.uni-koeln.de/dictyostalium/project.shtml
Funding
Agency: Deutsche Forschungsgemeinschaft (DFG).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Deutsche Forschungsgemeinschaft (DFG). Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /organism="Dictyostelium discoideum"
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SGS

CDS

VMS.IPKTIVNKWRCTVNNDHOKEGGSGGGSGGTIKSLPESCIVILNYPFEMIIQTKY
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Hall, N., Pain, A., Berriman, M., Churcher, C., Harris, B., Harris, D., Mungall, K., Bowman, S., Atkin, R., Baker, S., Barron, A., Brooks, K., Bucke, C.O., Burrows, C., Cherevach, I., Chillingworth, T., Christodoulou, Z., Clark, L., Clark, R., Corton, C., Crolin, A., Davies, R., Davis, P., Dear, P., Dearden, F., Doggett, J., Feltwell, T., Gobbe, A., Goodhead, I., Ganilliam, R., Hanlin, N., Hance, Z., Harper, D., Hauser, H., Hornsby, T., Holroyd, S., Horrocks, P., Humphray, S., Jagels, K., James, K.D., Johnson, D., Kerhornou, A., Knights, A., Konfortov, B., Kyes, S., Larke, N., Lawson, D., Lawson, D., Price, C., Quail, M.A., Rubler, S., Murphy, L., Oliver, K., Ormond, D., Price, C., Quail, M.A., Sanders, M., Simmonds, M., Seeger, K., Sharp, S., Smith, R., Squares, S., Stevens, K., Taylor, K., Tivey, A., Unwin, L., Whitchead, S., Woodward, J., Sulston, J.E., Craig, A., Newbold, C. and Barrell, B.G.

L. Nature, 419 (6906), 527-531 (2002)
                                                                                                                                                                                                                                                                                         Plasmodium falciparum strain 3D7, chromosome 5, segment 3/4.
AL929353 AL644504
AL929353.1 GI:23504644
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/db_xref="G1:23504645"
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DLFPSSLYPPYBIIIFTTAIKSYADTVLNIIDVDHYIDKKFYREDCYEMNEKLYIKNL
Submitted (20-SEP-2002) P.falciparum Genome Sequencing Consortium, The Welcome Trust Sanger Institute, Wellcome Trust Genome Campus, Hinxcon, Cambridge CB10 1SA, UK
For more information about this sequence or the Malaria Project, see http://www.sanger.ac.uk/Projects/P_falciparum.
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complement(148. .1134)
/gene="Pro795c" | figure | figure | figure | figure | figure | figure | figure | figure | figure | figure | figure | figure | figure | figure | figure | figure | figure | figure | figure | figure | figure | figure | figure | figure | figure | figure | figure | figure | figure | figure | figure | figure | figure | figure | figure | figure | figure | figure | figure | figure | figure | figure | figure | figure | figure | figure | figure | figure | figure | figure | figure | figure | figure | figure | figure | figure | figure | figure | figure | figure | figure | figure | figure | figure | figure | figure | figure | figure | figure | figure | figure | figure | figure | figure | figure | figure | figure | figure | figure | figure | figure | figure | figure | figure | figure | figure | figure | figure | figure | figure | figure | figure | figure | figure | figure | figure | figure | figure | figure | figure | figure | figure | figure | figure | figure | figure | figure | figure | figure | figure | figure | figure | figure | figure | figure | figure | figure | figure | figure | figure | figure | figure | figure | figure | figure | figure | figure | figure | figure | figure | figure | figure | figure | figure | figure | figure | figure | figure | figure | figure | figure | figure | figure | figure | figure | figure | figure | figure | figure | figure | figure | figure | figure | figure | figure | figure | figure | figure | figure | figure | figure | figure | figure | figure | figure | figure | figure | figure | figure | figure | figure | figure | figure | figure | figure | figure | figure | figure | figure | figure | figure | figure | figure | figure | figure | figure | figure | figure | figure | figure | figure | figure | figure | figure | figure | figure | figure | figure | figure | figure | figure | figure | figure | figure | figure | figure | figure | figure | figure | figure | figure | figure | figure | figure | figure | figure | figure | figure | figure | figure | figure |
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Devlin,K., Baker,S., Davies,P., Mungal,K., Berriman,M., Pain,A.,
Hall,N., Bowman,S., Churcher,C., Quail,M. and Barrell,B.
Direct Submission
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/organism="Plasmodium falciparum 3D7"
/mol type="genomic DNA"
/isolate="3D7"
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/chromosome="5"
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/gene="PFE0795c"
                                                                                                                                                                         147 AAGCAACGCTTGAAAAAAGGAAA 169
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Plasmodium falciparum 3D7
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                                                                                      CPRLHDHYEGTEKRYQLQYAIRDAKYTASDENIKLMPQPNIRLDILHEIGYIDDENTV
TKGRVSREIBINCEDLVITELIFRDAFINLESBENSVILSCLIFQEKNOVDSEIPPRL
EEAKONLIKTARKYKYKUSDKGLDVVPDDKLETTIKPGLMQVVYBMAGTPPRDICTI
TNVLEGSIVRAITRIGETCQEVRNAARVIGDTKLLQKMEBAMRLIKRDIVFTSSLYVN
                                 SLKLKI ENDI VLCVGNEI ITSSGGKEIMKVCNEKLQLKQSDLKSILAGAESGGESEIL
INSLEQQLLRLIEEYPLPLGPKSI DPI KQLKLKDVDFVSTYDHLQSI EKLI PESKCHK
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SSNIEKEVNDDDDDDDDNNDDDEIFENEKYTIGLILECKSTLIKQYTNTKVDRVFKIF
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complement(join(20381. .22148,22235. .23160,23330. .23685,
24790. .24793))
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                                                                                                                                                                                                                                                                               /norde="GeneilD exon scores" (in order of location ranges):
41.07 - GSCJ ID dd_02896"
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/product="similar to Involved in global regulation of
rranscription; Snf5p [Saccharomyces cerevisiae]"
/protein id="AAOS1182.1"
/db_xref="G1:28828579"
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   27 ITTATATGCTGATTTATGGGTGATTTTGCTTCCTTCTTTATACTTTTATTTTTATTCCCAAA
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Genes, compositions, kits, and methods for identification,
assessment, prevention, and therapy of cervical cancer
patent: WO 0142467-A 2746 14-JUN-2001,
Millennium Predictive Medicine, Inc. (US)
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Pred. No. 1.9;
0; Mismatches
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Pred. No. 1.3;
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/mol_type="genomic DNA"
/db_xref="taxon:9606"
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Best Local Similarity 54.4%;
Matches 98; Conservative
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AX187051
LOCUS
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AUTHORS
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RYYYI KKKMI FVBLY FNINYPPSYMILMCTGLRUBKLI NDRKI LYGECMLNIK KESDFI
ILLPKEI IMAP FFI FOI FMI LWFPSYMILMCTGLRUBKLI NDRKI LYGECMLNIK KESDFI
ILLPKEI IMAP FFI FOI FMI LWSTANTHACTBY SI ILLELATT KNOKKI KN
MLNYTCPINYPR YNTSY I 18SSEL VPGDI YEI KONMTI PCDTI ILLSGSYTWEBENTIG
KORBY KSNTHDLCSMYLCY INNYT DDVHAKNNKONTNNNNNNKKKKKI NNL FVKGI
YINSNDLLYDDKIGYNI FEBDVYNMKTRENNOYNNNNNNKKKKKI NNL FVKGI
YINSNDLLYDDKIGYNI FSBDYNNMKTRENNOYNNNNNNKKERNI LGLY ITGGF
ITTKGKI YNNI LYHKKELNLI NDSYKPLI ILLI I TA FPSYPILLY ITLSNNBYTNHI I
IKCLDI ITDA I PPALPYTTYNGY SI A I SRLKKKFSI SCLCPHKINI AGGINTWNPPDKT
GTLTENNLOP IGI I TONKKNRML SDFI HI KENNTESY HEKKKEY YTNNTYNDENT
IKDNMKNLHTSSKKKI I TKERSPLYOP Y KSCLLKOHY I KEKKKEY YTNNTYNDENT
NDSYCSSYLLANSETKOA Y CESYYNI DHLCDINKKMDINSKNBLAGKYS SKNELMGKYSK
NELMGKYI KNBELMGKYS KNBELMGKY SKNBLMGKYSK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             / LEAN 12 OF 17 OF 17 OF 17 OF 17 OF 17 OF 17 OF 17 OF 17 OF 17 OF 17 OF 17 OF 17 OF 17 OF 17 OF 17 OF 17 OF 17 OF 17 OF 17 OF 17 OF 17 OF 17 OF 17 OF 17 OF 17 OF 17 OF 17 OF 17 OF 17 OF 17 OF 17 OF 17 OF 17 OF 17 OF 17 OF 17 OF 17 OF 17 OF 17 OF 17 OF 17 OF 17 OF 17 OF 17 OF 17 OF 17 OF 17 OF 17 OF 17 OF 17 OF 17 OF 17 OF 17 OF 17 OF 17 OF 17 OF 17 OF 17 OF 17 OF 17 OF 17 OF 17 OF 17 OF 17 OF 17 OF 17 OF 17 OF 17 OF 17 OF 17 OF 17 OF 17 OF 17 OF 17 OF 17 OF 17 OF 17 OF 17 OF 17 OF 17 OF 17 OF 17 OF 17 OF 17 OF 17 OF 17 OF 17 OF 17 OF 17 OF 17 OF 17 OF 17 OF 17 OF 17 OF 17 OF 17 OF 17 OF 17 OF 17 OF 17 OF 17 OF 17 OF 17 OF 17 OF 17 OF 17 OF 17 OF 17 OF 17 OF 17 OF 17 OF 17 OF 17 OF 17 OF 17 OF 17 OF 17 OF 17 OF 17 OF 17 OF 17 OF 17 OF 17 OF 17 OF 17 OF 17 OF 17 OF 17 OF 17 OF 17 OF 17 OF 17 OF 17 OF 17 OF 17 OF 17 OF 17 OF 17 OF 17 OF 17 OF 17 OF 17 OF 17 OF 17 OF 17 OF 17 OF 17 OF 17 OF 17 OF 17 OF 17 OF 17 OF 17 OF 17 OF 17 OF 17 OF 17 OF 17 OF 17 OF 17 OF 17 OF 17 OF 17 OF 17 OF 17 OF 17 OF 17 OF 17 OF 17 OF 17 OF 17 OF 17 OF 17 OF 17 OF 17 OF 17 OF 17 OF 17 OF 17 OF 17 OF 17 OF 17 OF 17 OF 17 OF 17 OF 17 OF 17 OF 17 OF 17 OF 17 OF 17 OF 17 OF 17 OF 17 OF 17 OF 17 OF 17 OF 17 OF 17 OF 17 OF 17 OF 17 OF 17 OF 17 OF 17 OF 17 OF 17 OF 17 OF 17 OF 17 OF 17 OF 17 OF 17 OF 17 OF 17 OF 17 OF 17 OF 17 OF 17 OF 17 OF 17 OF 17 OF 17 OF 17 OF 17 OF 17 OF 17 OF 17 OF 17 OF 17 OF 17 OF 17 OF 17 OF 17 OF 17 OF 17 OF 17 OF 17 OF 17 OF 17 OF 17 OF 17 OF 17 OF 17 OF 17 OF 17 OF 17 OF 17 OF 17 OF 17 OF 17 OF 17 OF 17 OF 17 OF 17 OF 17 OF 17 OF 17 OF 17 OF 17 OF 17 OF 17 OF 17 OF 17 OF 17 OF 17 OF 17 OF 17 OF 17 OF 17 OF 17 OF 17 OF 17 OF 17 OF 17 OF 17 OF 17 OF 17 OF 17 OF 17 OF 17 OF 17 OF 17 OF 17 OF 17 OF 17 OF 17 OF 17 OF 17 OF 17 OF 17 OF 17 OF 17 OF 17 OF 17 OF 17 OF 17 OF 17 OF 17 OF 17 OF 17 OF 17 OF 17 OF 17 OF 17 OF 17 OF 17 OF 17 OF 17 OF 17 OF 17 OF 17 OF 17 OF 17 OF 17 OF 17 OF 17 OF 17 OF 17 OF 17 OF 17 OF 17 OF 17 OF 17 OF 17 OF 17 OF 17 OF 17 OF 17 OF 17 OF 17 OF 17 OF 17 OF 17 OF 17 OF 17 OF 17 OF 17 OF 17 OF
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INDONYPIINNVYKKOCYNITWSFIVANYHKTHYRPOQIINITFLKRNPRENBAFK
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HDELINLLKNSFIISPOQYVEPYHNSPYIIDICLONOTSKIGYSIPGEKEYLMKSS
WDFWYTGIVTLQMRILHAHGWKIIPINAGEWLQLNFDQKKNLLSEYFKQYSIQI"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note="Similar to Plasmodium falciparum probable cation-transporting Afraes 1 SW+ATX1 PLAFA (Q04956) (1956 aa) facts governes: E(): 0, 97.919% id in 1970 aa Large N- and C-terminal extensions predicted by TWHPM2.0 at as 50-72, 286-308, 334-356, 361-380, 708-730, 2173-2195, 2207-2229, 2263-2282, 2302-2324 and 2334-2356"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TNI KKELSKI I LI DDSNI SGFQY PDNF FPIKKWQGDLNDNELLHLI PFFLNLRKLKDI
RSLCSFRLI SQKDVSKLLCTSSSKHI KYLTDDNSKYLYRHSLA FQAINYLKI FMNKFR
YASSKKQWNELGKKINNKLKSYPFSLSKLKGSSDDEHKKKHRKI INNRKMLR"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /product="cation-transporting ATPase 1"
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| VALVILLHYVPCYLENGLILLHINFFPFPRETRYRHYHSYCKYNEWYRYKENHYYPFRDQNIMWER
| KIKKIKENHYNCYWANDVFFSEDQSMSSMYNDKEQNINFEDNIMWER
| KONINLKOHIKLSGHINLKONIKLSGHINLKONIKLSGHINFKONI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GKYSKNELMGKTIKNOVGVDTNIYHMNCDNDYNYDYPCDYNCNNCNDTYHRLEYHNIN
KDNSFNIPPEKNKSYNNISEHIKINYPLLFEALACCHTLSKVNNKIMGDVLEILMFNF
TNCDMLINNNSFIIKEKKKNCSYDFQKIDGDKNIGANDERCHLNNNLVSYNILKRFEF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         join(7484. .14348,14522. .14859)
/gene="PFE0805w"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              join (7484. .14348,14522. .14859)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /product="hypothetical protein"
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|join(3549. .6704,6817. .6915)
|gene="PFE0800w"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       number="3.6.3.-"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 gene="PFE0805w"
                                                                                                                                                                                                                                                                                                                                                                                                                              codon_start=1
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gene

800

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NNILDCILGLIGYKYIHNNNNBHICNSYKVGDTDNYNNAHHNDYNGNNIKKYSTVQ
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NLSDEXQNCLLOCRISTHILSSSNDPPNDNICLSNDLPNDNICLSND
LPNDNICLSNDLPNDNICLSNDLPNDNICLSNDLPNDNICLSNDLPNDNICLSNDLPNDNICLSNDLPNDNICLSNDLPNDNICLSNDLPNDNICLSNDLPNDNICLSNDLPNDNICLSNDLPNDNICLSNDLPNDNICLSNDLPNDNICLSNDLPNDNICLSNDLPNDNICLSNDLPNDNICLSNDLPNDNICLSNDLPNDNICLSNDLPNDNICLSNDLPNDNICLSNDLPNDNICLSNDLPNDNICLSNDLPNDNICLSNDLPNDNICLSNDLPNDNICLSNDLPNDNICLSNDLPNDNICLSNDLPNDNICLSNDLPNDNICLSNDLPNDNICLSNDLPNDNICLSNDLPNDNICLSNDLPNDNICLSNDLPNDNICLSNDLPNDNICLSNDLPNDNICLSNDLPNDNICLSNDLPNDNICLSNDLPNDNICLSNDLPNDNICLSNDLPNDNICLSNDLPNDNICLSNDLPNDNICLSNDLPNDNICLSNDLPNDNICLSNDLPNDNICLSNDLPNDNICLSNDLPNDNICLSNDLPNDNICLSNDLPNDNICLSNDLPNDNICLSNDLPNDNICLSNDLPNDNICLSNDLPNDNICLSNDLPNDNICLSNDLPNDNICLSNDLPNDNICLSNDLPNDNICLSNDLPNDNICLSNDLPNDNICLSNDLPNDNICLSNDLPNDNICLSNDLPNDNICLSNDLPNDNICLSNDLPNDNICLSNDLPNDNICLSNDLPNDNICLSNDLPNDNICLSNDLPNDNICLSNDLPNDNICLSNDLPNDNICLSNDLPNDNICLSNDLPNDNICLSNDLPNDNICLSNDLPNDNICLSNDLPNDNICLSNDLPNDNICLSNDLPNDNICLSNDLPNDNICLSNDLPNDNICLSNDLPNDNICLSNDLPNDNICLSNDLPNDNICLSNDLPNDNICLSNDLPNDNICLSNDLPNDNICLSNDLPNDNICLSNDLPNDNICLSNDLPNDNICLSNDLPNDNICLSNDLPNDNICLSNDLPNDNICLSNDLPNDNICLSNDLPNDNICLSNDLPNDNICLSNDLPNDNICLSNDLPNDNICLSNDLPNDNICLSNDLPNDNICLSNDLPNDNICLSNDLPNDNICLSNDLPNDNICLSNDLPNDNICLSNDLPNDNICLSNDLPNDNICLSNDLPNDNICLSNDLPNDNICLSNDLPNDNICLSNDLPNDNICLSNDLPNDNICLSNDLPNDNICLSNDLPNDNICLSNDLPNDNICLSNDLPNDNICLSNDLPNDNICLSNDLPNDNICLSNDLPNDNICLSNDLPNDNICLSNDLPNDNICLSNDLPNDNICLSNDLPNDNICLSNDLPNDNICLSNDLPNDNICLSNDLPNDNICLSNDLPNDNICLSNDLPNDNICLSNDLPNDNICLSN
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complement (join(15807. .15912,16021. .16198,16441. .16612))
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /product="40S ribosomal subunit protein S14, putative"
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TDLSGRETLVRITGGMKVKADRDESSPYAAMMAAQDVAARLKELGVTAIHIKLRASGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /notes"Weak similarity to several tRNA pseudouridine synthases, incl. Staphylococcus aureus tRNA pseudouridine synthase a trua TR: BAB45147 (EMBL:AP003164) (267 aa) fasta scores: E(): 0.0011, 30.952% id in 126 aa Signal peptide predicted by SignalP 2.0 HWA (Signal peptide probabilty 0.925, signal anchor probabilty 0.071) with cleavage site probability 0.497 between residues 24 and 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                         EGRASLVNSPQLFKFISLYSIMQCSQVLILYSISNKLTDNQYIPIDIVTILPLSIFMC
THASASKLSKNIPIGKLFSPPILISTYQVIIQLFPVMISULLMMLSPFYKDDKNVW
KEKSDDTYLYKAQNTLLYICSPQNLPMCTSINIKNEWRKSVFTNTAFIIMMSFLLLM
NTCITPFSSEIFLVGWHIDLLKQYLSLITPPPYFRIPLFFILPFNIPCSYSYEKYIIK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  complement(join(15807. .15912,16021. .16198,16441. .16612))
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HNFECFRGTLKGTEKLRKINTFCTIHFLDVYELKNNLYQFVIQGDRFLYHMIRIIVGT
LVQVGVGLLNVEDVRDALHLCKPLKVKLCAPSQGLCLNKILLQEPLDKLIGSALISN"
                                                                                                                               TYTSNNIYLSKYKYVHKNYYYPDSCTNLRKKKNSLFYNLKKYIYYEKKKYLQHCLLK
HWYXKVELPRIKOINYSYQMESIKTNYFIHELSEQPAIFSNILLSFYTIKNDNNVY
HKNYIYNKYIYNKYYIYNKYSICKKNYIKNYRONIYNKONIYNKONITHAKSYLLSG
SSKKPLKFPSNIIRHKLKEKKNKKNIKRYKONHVNNTSKGHIILMCTHGFKKVYSG
                                                                                                                                                                                                                                                                                                                     LKNKYRI VNNKGYMLKNDNYYDRHMYNLTDMYRGTOYGCSKKKNKNI YMNNNNI LKN
KINRPLEHLLLVDKCKRNI CHKYTDI KNIKLBI YEYI LRTCTVYARMKPKDKSDLILSL
KKLPNNSYVGMCGDGANDCLALSCADIGISLCNNNESSICSSPTSNKLCLHSI VHILI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /notes"Similar to Arabidopsis thaliana putative 40s ribosomal protein 814 f24k9.19 TR:Q9CAX6 (EMBL:AC008153) (150 aa) fasta scores: E(): 2.9e-44, 81.457% id in 151 aa" /codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           l probable transmembrane helix predicted by TWHMM2.0 at aa
5-24"
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YEHRTNDIQPDKLCDILINKDPRNVNIVLTGKAPIPLKKKPYSPHLPYYBECKNIVHY
                                            I MKKKKKKKI KNI I NNHNSNLYYHYN I I DTFVKRMNKBYMCFNKLLYKI QQKLLYNLI H
NLYKKKKYMNYYD I DEVHLI GNNNNNKONNSKEKKLPLPLKNKMKHI RKNESNDN I TFN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     86
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     27 TITATATGCTGATTTATGGGTGATTTTGCTTCCTTCTTTATACTTTTATTTCCCAAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       84; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 3,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        complement (21428. .22435)
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Pred. No. 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        18908. .20953
/gene="PFE0815w"
18908. .20953
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /gene="PFE0810c"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   gene="PFE0810c"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 'gene="PFE0815w"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /gene="PFE0820c"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /gene="PFE0820c'
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INV 29-JAN-2003

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Hall,N., Pain,A., Berriman,M., Churcher,C., Harris,B., Harris,D.,
Mungall,K., Bowman,S., Atkin,R., Baker,S., Barron,A., Brooks,K.,
Buckee,C.O., Burrows,C., Cherevocach,I., Chillingworth,C.,
Chillingworth,T., Christodoulou,Z., Clark,L., Clark,R., Corton,C.,
Cronin,A., Davies,R., Davis,P., Dear,P., Dearden,F., Doggett,J.,
Feltwell,T., Goble,A., Goodhead,I., Gwilliam,R., Hamlin,N.,
Hance,Z., Harper,D., Hauser,H., Hornsby,T., Holroyd,S.,
Horrocks,P., Humphray,S., Jagels,K., James,K.D., Johnson,D.,
Kerhornou,A., Knights,A., Konfortov,B., Kyes,S., Larke,N.,
Lawson,D., Lennard,N., Line,A., Maddison,M., Mclean,J., Mooney,P.,
Moule,S., Murphy,L., Oliver,K., Ormond,D., Price,C., Quail,M.A.,
Rabbinowitsch,E., Rajandream,M.A., Rutter,S., Sutherford,K.M.,
Sanders,M., Simmonds,M., Seger,K., Sharp,S., Smith,R., Squares,R.,
Squares,S., Stevens,K., Taylor,K., Tivey,A., Unwin,L.,
Whitehead,S., Woodward,J., Sulston,J.E., Craig,A., Newbold,C. and
Barrell,B.G.
D. Nature 419 (6906), 527-531 (2002)
                                                                                                                                  PFWAL13F7
PERMAL13F7
PLOUR Plasmodium falciparum MAL13F7, complete sequence.

AL0134559 AL008974 AL008975 AL008981 AL008983 AL009015 AL010138
AL010143 AL010146 AL010154 AL010157 AL010160 AL010169
AL010187 AL010189 AL010208 AL010208 AL010214 AL021885 AL021888
AL139179 AL844502 Z98556 Z98557 Z98558
AL139179 AL844502 Z98556 Z98557 Z98558
AL139179 AL84502 Z98556 Z98557 Z98558
AL01345594 G1:8052278
S HTG; 405 Ribosomal Protein S3A; acyl transferase; cyclophilin; elongation factor; F84012.11-11ke protein; Head alongation factor; F84012.11-11ke protein; Head and alongation factor; F84012.11-11ke protein; Head alongation factor; F84012.11-11ke protein; Head arobatic repeat; repat; replat; replat; kinesin-related protein; steevor; T-complex protein; legilon subunit; telomere; var. Plasmodium falciparum 3D7
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Lawson, D., Bowman, S. and Barrell, B.
Direct Submission
Submitted (17-DEC-1998) P.falciparum Genome Sequencing Consortium,
The Sanger Centre, Wellcome Trust Genome Campus, Hinxton, Cambridge
CB10 1SA, UK
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1 (bases I to 253305)

Bowman,S., Lawson,D., Basham,D., Brown,D., Chillingworth,T.,

Churcher,C.M., Craig,A., Davies,R.M., Devlin,K., Peltwell,T.,

Gentles,S., Gwilliam,R., Hamlin,N., Harris,D., Holroyd,S.,

Hornsby,T., Horrocks,P., Jagels,K., Jassell,B., Kyes,S., McLean,J.,

Moule,S., Mungall,K., Murphy,L., Oliver,K., Quall,M.A.,

Rajandream,M.-A., Rutter,S., Skelton,J., Squares,R., Squares,S.,

Sulston,J.E., Whitehead,S., Woodward,J.R., Newbold,C. and

Barrell,B.G.

The complete nucleotide sequence of chromosome 3 of Plasmodium
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AQIRRRRYA II FFENAAAVRKA I DLFNEKEVLGAKVTVSPAKT SPKPDPHEGSSVVFL
SPI FRMSTTNGQI RELFTGMRVLRI RTYRQNYAYVYLDSAAAAQKFVKEKNGTEFRGK
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Zhang, J. and Williams, N.
Direct Submission
Submitted (24-AUG-1997) Microbiology, State University of New York
at Buffalo, 3435 Main St., Buffalo, NY 14214, USA
Location/Qualifiers
   AF020696 1052 bp mRNA linear INV 21-OCT-199
Trypanosoma brucei RNA binding protein (TBP37) mRNA, complete cds.
AF020696
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Eukaryota, Buglenozoa, Kinetoplastida, Trypanosomatidae,
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/mol_type="mRNA"
/strain="TREU667"
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/protein_id="AAB81433.1"
/db_xref="GI:2554935"
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PUBMED
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/translation="MANTYDELYVPLSYYILQNEGGNTSKIDQANTKKPKKEVINKS
SLIIDIKPYGENTDLDEVLKLVKNITMEGLTWGKAHKKTPFAFGLFKLQVSCVIVDDL
VNTDELLETIETLENGGLDREQLGKKKQNDDDERNYDEDBIGGLVQSAEIISFNKL"
John (10556 . 10737,11044 . .11146,11373 . .20416,20578 . .20690)
                                                                                                                                                                                                                                                                                                                            /note="gynonym: PFC0875w"
join(10596. 10737,11044. .11146,11373. .20416,20578. .20690)
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                                                                                                                                                                                                                                                                                                                                                                                                 /note="Revised: added 3' exon, possibly spliced at 5' end, revised: added 2x 5' exons by similarity with P. knowlesi; signal anchor predicted by SignalP 2.0 HWM (Signal peptide probabilty 0.001, signal anchor probability 0.997) with cleavage site probability 0.000 between residues 36 and 37 Pfam match to entry PP00005 ABC_tran, ABC transporter, score 72.50, E-value 9e-18"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1.1e-15, 53.2% identity in 141 as overlap, revised:
shortened exon 2, splicing confirmed in P. knowlest; Pfam:
match to PP00736 EF1BD, EF-1 guanine nucleotide exchange
domain Score 61.10, B-value 7.9e-22"
/codon start=1
/product.=longation factor 1 (EF-1); putative"
/db_xref="G1:8052274"
/db_xref="G1:8052274"
/db_xref="G1:8052274"
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ILVTNINEFTNNRDIIKKNIIKFIKGTRNENKNCPIPFNENHIYCTYKINELESLKKL
LCVLNKFKNILTYQLKTIDIYYTXIYIYTLNEKKKLLKNIQDKDIKYLIBIDPLFPLF
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MYNNHNKYGKYKNNNNNNSPYNARDDTELTDIEBNISSKKKKNKFIEKEFSYNTYRNN
KNNDENDEYGBYDNYDDNMIMSNTSNIMKKKNIKKONIPKTTYIKPTIKL
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/protein_id="CAB39024.3"
/db_xref="G1:23477031"
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57.1%; Pred. No. 1.6;
*ive 0; Mismatches
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Best Local Similarity 57.1
Matches 88; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               /translation="MCLPDKIRNIEKLNEAELKNIGNNDSSWHDOYRDSSYIVIGNLD
NRLTEGDIVIVFSQYGEFIDVNLVRDNETGKSKGYCFLSYADQRSTILAVDNFNGYKL
LERPLVVDHILNYRLPKKYLKDADKNEYKPTGAEGQGIGVYNVVESEIKLSKVFDKIK
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DDBDDDDDSVDI KYKRHKEKRKSLTTKKYDKKEKHKRKSDHRDKHRRRENHSRHREK
EKDKKSHKRRHKHSYDKYSSRSRSYSTSSSTDR."
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join (5457. .5577,5689. .5787,5923. .6077,6189. .6743)
/gene="MALJP7.2"
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|gene="MAL3P7.2"
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/note="Similarity: to kinesin-related protein.
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gene="MAL3P7.3"
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/protein id="CAB13067.1"
/b_xref="G1:4494008"
/db_xref="G0A:097318"
/db_xref="SPTREMBL:097318"
                      falciparum 3D7"
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|gene="MAL3P7.3"
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/product="Kinesin, putative"
/protein id="CAB39023.1"
/db_xref="G1:4493964"
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                                                                                                                                                                                       note="synonym: PFC0860w"
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mol type="genomic DNA"
isolate="3D7"
                                                                             db_xref="taxon:36329"
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/clone="MAL3P7"
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gap of 100 bp
contig of 953 bp in length
gap of 100 bp
contig of 1010 bp in length
gap of 100 bp
contig of 1033 bp in length
gap of 100 bp
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3: contig of 973 bp in length
1: gap of 100 bp
2: contig of 942 bp in length
3: gap of 100 bp
                                                                     8: gap of 100 bp
5: contig of 927 bp in length
5: gap of 100 bp
6: contig of 979 bp in length
7: gap of 100 bp
                                                                                                                                                             4: gap of 100 bp

9: contig of 875 bp in length

9: gap of 100 bp

1: contig of 991 bp in length

9: gap of 100 bp
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contig of 944 bp in length
gap of 100 bp
contig of 947 bp in length
gap of 100 bp
contig of 950 bp in length
gap of 100 bp
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contig of 931 bp in length
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contig of 961 bp in length
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contig of 912 bp in length
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72 38971: gap of 100 bp
72 39989: contig of 1018 bp in length.
Location/Qualifiers
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contig of 969 bp in length
gap of 100 br
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of 1008 bp in length
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contig of 964 bp in length
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of 901 bp in length
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of 903 bp in length
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                                                                                                                                    ACU91136
39989 bp DNA linear HTG 28-NOV-2001
HOMO Bapiens chromosome 11 clone RP5-873F21 map 11, LOW-PASS
SOCIENCE SAMPLING.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Submitted (01-APR-2001) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA ON NOv 22, 2001 this sequence version replaced gi:13493100. All repeats were identified using RepeatMasker: Smit, A.F.A. & Green, P. (1996-1997) http://ftp.genome.washingcon.edu/RM/RepeatWasker.html
                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. I (bases I to 3989)
Birren, B., Linton, L., Nusbaum, C. and Lander, E. Homo gaplens chromosome 11, clone RPS-873F21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ------ Genome Center Center: Whitehead Institute/ MIT Center for Genome Research
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* sequencing reads that have not been assembled into
contigs. Runs of N are used to separate the reads
* and the order in which they appear is completely
arbitrary. Low pass sequence sampling is useful for
* identifying clones that may be gene-rich and allows
* overlap relationships among clones to be deduced.
* However, it should not be assumed that this clone
* will be sequenced to completion. In the event that
* the record is updated, the accession number will
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Contact: sequence_submissions@genome.wi.mit.edu
------- Project Information
Center project name: 1.12134
Center clone name: 873_F_21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              938: contig of 938 bp in length
1038: gap of 100 bp
2183: contig of 1145 bp in length
                           35400 AAAAAAAAAAGGGAAAAATGAAAATTACATTA 35367
    146 AAAGCAACGCTTGAAAAAGGAAAGTTAGCCCTA 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Center code: WIBR
Web site: http://www-seq.wi.mit.edu
                                                                                                                                                                                                                                               AC091136.2 GI:17047133
HTG; HTGS PHASE0.
HOmo sapiens (human)
Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (bases 1 to 39989)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  Unpublished
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KEYWORDS
SOURCE
ORGANISM
                                                                                                                 RESULT 22
AC091136/c
                                                                                                                                                             LOCUS
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JOURNAL
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AUTHORS
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Barna, N., Bastien, V., Baloam, T., Boguslavkiy, L., Boukhgalter, B., Camarata, J., Charag, J., Chazaro, B., Choepel, Y., Collymore, A., Camarata, J., Charg, J., Chazaro, B., Choepel, Y., Collymore, A., Cook, A., Cook, A., Cook, A., Cook, A., Cook, A., Cook, A., Cook, A., Cook, A., Cook, A., Cook, A., Cook, A., Cook, A., Carham, L., Grand-Pierre, N., Hagos, B., Hadre, M., Iliev, C., Mant, A., Karatas, A., Kells, C., Landers, T., Levine, R., Lindblad-Toh, K., Liu, G., MacLean, C., Macdonald, P., Major, J., Machan, C., Macdonald, P., Mhova, T., Menga, V., Murphy, T., Naylor, J., Nguyen, C., Nicol, R., Norbu, C., Norman, C., Phunkhang, P., Plerre, N., Raymond, C., Retta, R., Rise, C., Spencer, B., Stange-Thomann, N., Stojamovic, N., Talamas, J., Tasfaye, S., Thopsan, M., Vosh, W., Wille, R., Wo, A., Willson, B., Wux, X., Wyman, D., Young, G., Zainoun, J., Vosh, W., X., Wyman, D., Young, G., Zainoun, J., Zainer, A. and Zody, M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Direct Submission
Submitted (06-MG-2002) Whitehead Institute/MIT Center for Genome
Submitted (106-MG-2002) Whitehead Institute/MIT Center for Genome
Research, 320 Charles Street, Cambridge, MA 02141, USA
On Aug 6, 2002 this sequence version replaced gi:12740251.
All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ------ Genome Center
Center: Whitehead Institute/ MIT Center for Genome Research
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Web site: with the contact: sequence_submissions@genome.wi.mit.edu
Contact: sequence_submissions@genome.wi.mit.edu
Contact: sequence_submissions@genome.wi.mit.edu
Contact: sequence_submissions@genome.wi.mit.edu
Contact: sequence_submissions@genome.wi.mit.edu
Center project Information
Sequencing vector: M13, M7815, 4% of reads
Sequencing vector: M13, M7815, 4% of reads
Sequencing vector: M13, M7815, 100% of reads
Sequencing vector: M13, M7815, 100% of reads
Sequencing vector: Plasmid; n/a; 96% of reads
Chemistry: Dye-terminator Big Dye, 100% of reads
Assembly program: Phrap; version 0.960731
Consensus quality: 145569 bases at least Q30
Consensus quality: 145569 bases at least Q30
Consensus quality: 145569 bases at least Q30
Consensus quality: 145569 bases at least Q30
Losert size: 145760; sum-of-contigs
Quality coverage: 8.2 in Q20 bases
Augusta of Secontigs Garét' sequence. It currently
consists of Secontigs Garét' sequence. It currently
consists of Secontigs Garét' sequence. It currently
consists of the gaps between them are based on estimates that have
provided by the submittor.
This sequence will be replaced

the days between them are based on estimates that
the accession number will be preserved.

the accession number will be preserved.

1 49524 43523; gap of 100 bp
51343 55402: contig of 1950 bp in length
55403 55502: gap of 100 bp
55403 55502: gap of 100 bp
55403 55502: gap of 100 bp
55403 55502: gap of 100 bp
55403 55502: gap of 100 bp
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /clone lib="RPCI-11 Human Male BAC"

    146150
    organism="Homo sapiens'
/mol_type="genomic DNA"

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /clone="RP11-222M17"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Center code: WIBR
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51443
55403
55503
93447
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      39206 AAAACAGAGCTTCATTTTACAATGACAGACCCCTTTATCCTGAGATAGGAAAAGGGGGAAA 39147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    39386 Arcacraraccrearrardaardarrirrarrirccrircriarargarricrcrara 39327
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         39326 CATTATGCAATAAACATATTTACTTTTATTAAAATAGTATCATAGGAAAAAAGGGAA 39267
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              39266 AACGTCACTACATTGAGTATTATGACACAAAATTCTTGTATTTAGATTGCTACTCTCCAC 39207
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ACC21298
Homo sapiens chromosome 11 clone RP11-222M17 map 11, WORKING DRAFT SECUENCE, 5 ordered pieces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   86 ATTITICITAAGCAAATATITI-CITIGCIAATCAATAAATTATCAAAAGAAAAAAACT 144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               204
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        145 GAAAGCAACGCTTGAAAAAAAGGAAAGTTAGCCCTATCGGGTATATTTTGGAAGTTGTAAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                          1;
                                                                                                                                                                                                                                                                                                                                                                       DB 2; Length 39989;
                                                                                                                                                                                                                                                                                                                                                                    Query Match
9.1%; Score 48.2; DB 2; Length 399
Best Local Similarity 52.3%; Pred. No. 1.9;
Matches 127; Conservative 1; Mismatches 114; Indels
                                                                                                                                                                                                                                                                         3932 others
                                                                                                                                                                                         /GCIONE="RPS-873F21"
/clone_lib="RPCI Human PAC library 5"
8024 c 7083 g 10567 t 3932 oci
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 (bases 1 to 146150)
Birren, B., Nusbaum, C. and Lander, E.
Homo sapiens chromosome 11, clone RP11-222M17
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HTG; HTGS PHASE2; HTGS_DRAFT; HTGS_FULLTOP.
HOMO sapiens
                                      organism="Homo sapiens"
                                                                  /mol_type="genomic_DN/
/db_xref="taxon:9606"
                                                                                                                                    chromosome="11"
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                                                                                                                                                                /map="11"
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S Birren, B., Linton, L., Nusbaum, C., Lander, E., All, A., Allen, N.,
Buckranon, S., Barna, N., Bastien, V., Bloom, T., Boguslavkiy, L.,
Boukrgalter, B., Brown, A., Camarata, J., Campoplano, A., Chang, J.,
Chazaro, B., Choepel, Y., Colangelo, M., Collins, S., Collymore, A.,
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Micol, R., Norbu, C., Norman, C.H., O'Connor, T., O'Donnell, P.,
Nicol, R., Norbu, C., Norman, C.H., O'Connor, T., O'Donnell, P.,
Pollara, V., Raymond, C., Rette, R., Riebeck, M., Rise, C.,
Rogov, P., Roman, J., Rosetti, M., Roy, A., Santos, R., Schauer, S.,
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Homo sapiens chromosome 11, clone RP11-624D11, complete sequence.
AC124657
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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Birren, B., Nusbaum, C. and Lander, E.
Homo sapiens chromosome 11, clone RP11-624D11
                                                                                                                                  9.1%; Score 48.2; Di 52.3%; Pred. No. 1.8;
                                       clone end:SP6 vector side:left" 49624. 51342 /note="assembly_fragment"
                      'note="assembly_fragment
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Matches 127; Conservative
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AC124657/c
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Schupback, R., Seaman, S., Severy, P., Spencer, B., Stange-Thomann, N., Stojanovic, N., Straubas, N., Subramanian, A., Talanas, J., Treffilio, J. Toplama, K., Travers, M., Talanas, J., Treffilio, J., Theodore, J., Toplama, K., Travers, M., Talanas, J., Treffilio, J., Theodore, J., Toplama, K., Travers, M., Travis, N., Trigilio, J., Vensilievi, Viel. R., Vo. A., Wilson, B., Wu, X., Wyman, D., Ye, W.J., Voung, G., Zainoun, J., Zembek, L., Zimmer, A. and Zody, M.

Intect Submarsion

Sharian, Bastien, V., Boom, T., Zimmer, A. and Zody, M.

Research, 32 Charles Street, Cambridge, M. 02141, USA

Research, J., Challes, Street, Cambridge, M. 02141, USA

Research, S., Perreirs, P., FitzGerald, M., Gage, D., Galagan, J., Collymore, A., Candar, J., Challe, P., FitzGerald, M., Gage, D., Galagan, J., S., Dodge, S., Faro, S., Perreirs, P., FitzGerald, M., Gage, D., Galagan, J., Gook, P., Devar, P., Carad-Pierre, M., Halon, W., Maclis, C., Karden, C., Karden, C., Macden, C., Retalan, L., Grand-Pierre, M., Halon, W., Maclis, J., Machen, R., Lidabad, Toh, K., Liu, G., Maclen, C., Macdonald, P., Major, J., Matthews, C., Maclen, C., Machen, J., Mayen, C., Maclen, C., Retala, P., Maron, J., Roy, A., Schauer, S., Schupback, R., Seaman, S., Severy, P., Sumission, D., Wurth, J., Woy, A., Schauer, S., Schupback, R., Seaman, S., Severy, P., Sumission, B., Wilson, B., Waman, D., Young, G., Zainoun, J., Roy, A., Schauer, S., Schupback, R., Seaman, S., Severy, P., Sumission, B., Wu, X., Wyman, D., Young, G., Zainoun, J., Roy, A., Stenger, P., Petersen, C., Boom, T., Waman, D., Young, G., Zainoun, J., Candar, B., Macle, M., Sange-Thomann, W., Stojanovic, N., Talamas, J., Subback, R., Devar, C., Maclen, C., Maclen, C., Maclen, C., Maclen, C., Maclen, C., Maclen, C., Maclen, C., Maclen, C., Maclen, C., Maclen, C., Maclen, C., Maclen, C., Maclen, C., Maclen, C., Maclen, C., Maclen, C., Maclen, C., Maclen, C., Maclen, C., Maclen, C., Maclen, C., Maclen, C., Maclen, C., Maclen, C., Maclen, C., Maclen, C., Maclen, C., Maclen, C., Maclen, C., Mac
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The remainder overlaps accession number AL358944 (Sanger Centre
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Web site: http://www-seq.wi.mit.edu
Contact: sequence_submissions@genome.wi.mit.edu
------- Project_Information
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Center clone name: 624_D_11
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57259 CATTATGCAATAAACATATTTACTTTTATTAAAATAGTATCATAGGAAAAAAAGGAA 57200
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Homo sapiens chromosome 11 clone RP11-802012 map 11, WORKING DRAFT
SEQUENCE, 16 unordered pieces.
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Birren, B. Linton, L., Nusbaum, C., Lander, E., Abraham, H., Allen, N., Anderson, S., Baldwin, J., Barna, N., Bastlen, V., Beda, F., Boguslavkiy, L., Boukhgalter, B., Brown, A., Burkett, G., Campopiano, A., Castle, A., Choepel, Y., Colangelo, M., Collins, S., Collymore, A., Cooke, P., Dearellano, K., Dewar, K., Diaz, J.S., Dodge, S., Domino, M., Doyle, M., Ferreira, P., Fitzhugh, W., Gage, D., Galagan, J., Gardyna, S., Ginde, S., Goyette, M., Graham, L.,
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Birren, B., Linton, L., Nusbaum, C. and Lander, E. Homo sapiens chromosome 11, clone RP11-802012
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Pred. No. 1.8;
1; Mismatches 114; Indels
                                                                                                                                                                                                             / remin | 2.2466 | / remin | 2.2466 | / rpt family="LTR16c" | / rpt family="LTR16c" | / rpt family="LTR14c" | / rpt family="MLT1J1" | 2.2445 | . 2.3343 | / rpt family="MLT1J1" | / rpt family="MLT1J1" | / rpt family="MLT1J1" | / rpt family="MLT1J1" | / rpt family="MLT1J1" | / rpt family="MRSA" | / rpt family="MRSA" | / rpt family="MRSA" | / rpt family="MRSA" | / rpt family="(CAAA)n" | / rpt family="(CAAA)n" | / rpt family="(CAAA)n" | / rpt family="(CAAA)n" | / rpt family="(CAAA)n" | / rpt family="(CAAA)n" | / rpt family="(CAAA)n" | / rpt family="(SSS99) | / rpt family="(SSS99) | / rpt family="(SSS99) | / rpt family="(SSS99) | / rpt family="(SSS99) | / rpt family="(SSS99) | / rpt family="(SSS99) | / rpt family="(SSS99) | / rpt family="(SSS99) | / rpt family="(SSS99) | / rpt family="(SSS99) | / rpt family="(SSS99) | / rpt family="(SSS99) | / rpt family="(SSS99) | / rpt family="(SSS99) | / rpt family="(SSS99) | / rpt family="(SSS99) | / rpt family="(SSS99) | / rpt family="(SSS99) | / rpt family="(SSS99) | / rpt family="(SSS99) | / rpt family="(SSS99) | / rpt family="(SSS99) | / rpt family="(SSS99) | / rpt family="(SSS99) | / rpt family="(SSS99) | / rpt family="(SSS99) | / rpt family="(SSS99) | / rpt family="(SSS99) | / rpt family="(SSS99) | / rpt family="(SSS99) | / rpt family="(SSS99) | / rpt family="(SSS99) | / rpt family="(SSS99) | / rpt family="(SSS99) | / rpt family="(SSS99) | / rpt family="(SSS99) | / rpt family="(SSS99) | / rpt family="(SSS99) | / rpt family="(SSS99) | / rpt family="(SSS99) | / rpt family="(SSS99) | / rpt family="(SSS99) | / rpt family="(SSS99) | / rpt family="(SSS99) | / rpt family="(SSS99) | / rpt family="(SSS99) | / rpt family="(SSS99) | / rpt family="(SSS99) | / rpt family="(SSS99) | / rpt family="(SSS99) | / rpt family="(SSS99) | / rpt family="(SSS99) | / rpt family="(SSS99) | / rpt family="(SSS99) | / rpt family="(SSS99) | / rpt family="(SSS99) | / rpt family="(SSS99) | / rpt family="(SSS99) | / rpt family="(SSS99) | / rpt family="(SSS99) | / rpt family="(SSS99) | / rpt family="(SSS99)
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complement (21582. .21799)
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complement(22347. .22
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AC068749.2 GI:8389606
HTG; HTGS PHASE1; HTGS_DRAFT.
HOMO BADIENB (human)
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Best Local Similarity 52.3%;
Matches 127; Conservative
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4976 98366: contig of 13391 bp in length

8367 98466: gap of 100 bp

3467 117242: contig of 18776 bp in length

7343 117342: gap of 100 bp

7343 147820: contig of 30478 bp in length

7821 147920: gap of 100 bp

1921 181996: contig of 34076 bp in length.

Location/Qualifiers
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/note="assembly_fragment"
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Matches 127; Conservative
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Grand-Pierre, N., Grant, G., Hagos, B., Heaford, A., Horton, L.,
Howland, J.C., Iliev, I., Johnson, R., Jones, C., Kann, L., Karatas, A.,
Klein, J., LaRocque, K., Lud, G., Locke, K., Macdonald, P., Marquis, N.,
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Murphy, T., Maylor, J., Mihova, T., Miranda, C., Mlenga, V., Morrow, J.,
Murphy, T., Naylor, J., Norman, C. H., O'Connor, T., O'Donnell, P.,
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Stange-Thomann, N., Stojanovic, N., Subramanian, A., Talamas, J.,
Tesfaye, S., Theodore, J., Tirrell, A., Travers, M., Trigilio, J.,
Vassiliev, H., Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Ye, W.J.,
Direct Submission Whitehead Institute/MIT Center for Genome
Submitted (08-MAY-2000) Whitehead Institute/MIT Center for Genome
Research, 320 Charles Street, Cambridge, MA 02141, USA
On Jun 9, 2000 this sequence version replaced gi:7717156.
All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997)
http://ftp.genome.washington.edu/RM/RepeatMasker.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NOTE: This is a 'working draft' sequence. It currently consists of 16 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
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Insert size: 180496; sum-of-contiga
Quality coverage: 4.5 in Q20 bases; agarose-fp
Quality coverage: 4.5 in Q20 bases; sum-of-contigs
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100 bp
9 of 5134 bp in length
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of 13941 bp in length
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PTNSFRKSTYGSVSSPSSSNKDSIKLGDEPAIREALKEFRSDENDIDWVLFGYEGGNS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ILRSSSSPSSESDEYSNGNNNNNS IINDLSSSSSSSSSSSSSSSITSPSSNHAYS
PYNRSHKGIKISPNNKQVSSSGLLGSTWVSTSLIMGASNINNNNNNNNNNNNNNNNNNNNN
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1.55, 2.07 - GSCJ_ID dd_00861"
/codon_start=1
CDS predictions from GeneID do not necessarily reflect true genes.
Purther Information is available from IMB Jena, Department of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 complement (join(10316. .11073,11163. .11973))
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (Slime
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /product="similar to Dictyostelium discoideum
mold). Homeobox-containing protein (Fragment)"
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/db_xref="GI:28829237"
                                                                                    and the Univerity Colonge, Institute for Biochemistry (http://www.uni-koeln.de/dictyostellum/project.shtml Funding
                                                                                                                                                           Deutsche Forschungsgemeinschaft (DFG)
Location/Qualifiers
                                                                                                                                                                                                 (http://genome.imb-jena.de/dictyostelium/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                'product="hypothetical protein"
                                                                                                                                                                                                                                                                                                  'db_xref="taxon:44689"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       205 ATACTACRIGITCTCTTAAGICCCACTCCTCTGTTTTCTTTGAGCAGGAAAGAGAAAG 264
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Nature 418 (6893), 79-85 (2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Mycetczoa; Dictyostellida; Dictyostellum.
1 (bases 1 to 36188)
Gloeckner, G., Eichinger, L., Szafranski, K., Pachebat, J., Dear, P.,
Edmann, R., Baumgart, C., Parra, G., April, J.F., Guigo, R., Kumpf, K.
Tunggal, B., Cox, E., Quail, M.A., Platzer, M., Rosenthal, A. and
Noegel, A.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Submitted (04-MAR-2003) Genome Analysis, Institute of Molecular Biocechnology, Beutenberstr. 11, Jena 07745, Germany 4 (bases 1 to 36188)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Submitted (21-MAR-2002) Genome Analysis, Institute of Molecular Biotechnology, Beutenberstr. 11, Jena 07745, Germany 3 (bases 1 to 36188)
                                                                                                                                                                                                                                                                                                                                            26 ATTIATATGCTGATTIATGGGTGATTTTGCTTCCTTCTTTATACTTTTATTTCCCAA
                                                                                                                                                                                                                                                                                                  Gape
                                                                                                                                                                                                                                                   Length 256221;
                                                                                                                                                                                                                                                                                                  7
                                                                                                                                                                                        2101 others
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Pred. No. 1.8;
1; Mismatches 114; Indels
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                     /note="assembly_fragment:01174
fragment_chain:1"
248608. 256221
/note="assembly fragment:06229
fragment_chain:1
clone_end:r7
vector_side=right"
a 51050 c 48305 g 76442 t 21
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Dictyostellum discoideum
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Best Local Similarity 52.3%;
Matches 127; Conservative
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248507: contig of 111471 bp in length 248607: gap of 100 bp 256221: contig of 7614 bp in length.
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119039: gap of 100 bp
129647: contig of 10608 bp in length
129747: gap of 100 bp
138936: contig of 7189 bp in length
137036: gap of 100 bp
                                                                22137 bp in length
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of 3786 bp in length
100 bp
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of 2097 bp in length
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52652. .56791
/note="assembly_fragment:02491.0"
56892. .65133
/note="assembly_fragment:02823"
6234. .67244
/note="assembly_fragment:03451"
67345. .69441
/note="assembly_fragment:03517"
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6466. 38014
force="assembly_fragment:01016"
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.16375. .118939
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119040. .129647
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/db_xref="taxon:9606"
/chromosome="11"
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                                                                                                                                            AL356371 256221 bp DNA 'linear HTG 20-OCT-2001 Homo sapiens chromosome 11 clone RP1-13519, *** SEQUENCING IN PROGRESS ***, 22 unordered pieces.
9926 AAAACAGAGCTTCATTTTACAATGACAGACCCCTTTATCCTGAGATAGGAAAGGGGGAAA 9985
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Assembly program: XGAP4; version 4.5
Assembly program: XGAP4; version 4.5
Assembly program: XGAP4; version 4.5
Sequencing vector: M13; M7815; 11* of reads
Sequencing vector: plasmid; L08752; 18* of reads
Chemistry: Dye-terminator ET-amersham; 2* of reads
Chemistry: Dye-terminator ET-amersham; 2* of reads
Consensus quality: 250899 bases at least Q40
Consensus quality: 252999 bases at least Q20
Consensus quality: 252999 bases at least Q20
Insert size: 254121; sum-of-contigs
Insert size: 354121; sum-of-contigs
Unsert size: 38381; 1.2* error; agarose-fp
Quality coverage: 9.35x in Q20 bases; sum-of-contigs Quality
coverage: 25.82x in Q20 bases; agarose-fp
                                                                                                                                                                                                                                                                                                                                                          Submitted (16-OCT-2001) Sanger Centre, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk On Jun 28, 2001 this sequence version replaced gi:14529810.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NOTE: This is a 'working draft' sequence. It currently consists of 22 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
                                                                                                                                                                                                                                                                            Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Butelo
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo
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Web site: http://www.sanger.ac.uk
                                                                                                                                                                                             .AL356371
AL356371.18 GI:14575185
HTG; HTGS PHASE1; HTGS_CANCELLED.
Homo sapiens (human)
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Direct Submission
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52652
                                265 CAG 267
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                                                                                                                                                                                                            VERSION
KEYWORDS
SOURCE
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                                                                                                                                                             DEFINITION
                                                                                                                                                                                             ACCESSION
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AUTHORS
TITLE
JOURNAL
                                                                                                               RESULT 26
                                                                                                                             AL356371
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TNYLFLGDYVDRGYFSMEVIIYLYACKINYPNTFFLLRGNHECRHLTEYFTFKEECLH
KYSERVENDPITESFNALPLAALMNGKFLCHGGLSPDIKTLDDIANIDRFKEPESGP
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AGYKCHLQNDATGFPSVITLERAPNYLDAYNNKGAVLRYENNVANIRQFTCSPHFWL
PNFWDVFTWSMPFVSEKTAEMLLVLLNLCNDEAAEKNGNALSVIRAHEAQN
KYGSVSRMRAFFSLLRQERETIMMIKSFSPSRFRIPGGLLTGGKDALKKALGDFAQARK
MDLINEKRPPILDRVNSRGELRMYSRGELRPINSKODLFRGNSYADLKPPGGPQFII
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/codon start=1
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/codon start=1
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Complement (join(7310. .7685,7804. .8195))

Complement (join(7310. .7685,7804. .8195))

21.45, 37.54 - GSCJ_ID dd_02158"

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                                                                                                                                                                                                                                                                                                                                                                                                           LGPMSTGSPATDERLINGALDGGASQSASWSSVEDCDASEIENEPPVVGECLPMD
GDYYYYYTYRVDYTNGTISKTAXSDDRCETPSRVEHFKIDECVKDCKLSGPYLFTIID
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SGSYIYTIIDSSEIVIPKOTLVVFDYTGECGVNWNQTPTTIRYTPINRCLLTSESTAY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PPYSYNQNNCIRYSEIEHRTGVQYKKEFNQQAFCNV"
join(11499. .11901,12090. .12332,12446. .12573,12727. .138
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34.04, 18.44, 14.18, 134.07 - GSCJ_ID dd_00246"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       complement(18695. .20509)
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117.34 - GSCJ ID dd_00251"
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(protein_id="AAOS0952.1"
(db_xref="GI:28828288"
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DNDNYXYYIYRVDYANGTISKTAYTEDRCQTFYSIEHFKIDECWNDCKLSGSYIYTII
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complement(join(5915...6290,6400...6732,6912...6940,
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YRCRNDDSSGLGPMSTGSFATDERMLNLGNIDGGNSQSASWSSSIQDCDNSEIENELF
IVVGECLLLDNDDFYYYIYRIDYANGTISKTGYTEDRCQNFYSIEHFKIDECVMDCKL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /product="gimilar to Homo sapiens (Human).
Phosphatidylinositol-glycan-specific phospholipase D 2
pecursor (EC 3.1.4.50) (PI-G PLD) (Glycoprotein
phospholipase D) (Glycosyl- phosphatidylinositol specific
phospholipase D)
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// note="GeneID exon scores" (in order of location ranges):
21.67, 38.95, -1.76, -1.75 - GSCJ_ID dd_02157"
// codon_gearer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     join(1227. 1359,1507. 1905,1986. .4300)
/note="GeneID exon scores (in order of location ranges):
2.23, 56.16, 218.21 - GSCJ_ID dd_02155"
                                  Direct Submission
Submitted (12-MR-2003) Genome Analysis, Institute of Molecular
Subchnology, Buttenberstr. 11, Jena 07745, Germany
On or before Mar 4, 2003 this sequence version replaced
g1:20067113, g1:20087115, g1:20087117, g1:1956926.
CDS predictions from GeneID do not necessarily reflect true gene
Purther Information is available from IMB Jena, Department of
                                                                                                                                                                                                                                                                                                                                 Genome Analysis
(http://genome.imb-jena.de/dictyostalium/)
and the Univerity Colonge, Institute for Biochemistry
(http://www.uni-koeln.de/dictyostalium/project.shtml
Punding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Agency : Deutsche Forschungsgemeinschaft (DFG) Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  'organism="Dictyostelium discoideum"
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chromosome="2"
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FWNHLIYBVSRYNHFYSTIINGDNLANSKIDIFKELIFGIYNTINRSHEEVLANEENEYA
                                                                                                                   I KDVRSDSTDTNWCLVGYKNDTTLTVIAKGNGGVDELVGHLNSKI VAYGLVREVERFD
LSDTI KFAFI DFVGED I NRMFRAKLGTHSGTVKQL FHPYHVDLHVSSPSELSSE LYTK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /trānslation="MDEDNNDRIEFLFWKVFRNKYIFNEIFYIIKNTEWVQYIDPSEI NIDNKCSIFETYSFELMFLKRYDDK NIDNKCSIFETYSFELMFLKRYDDDK NIENKREFKKNOFEVKKVRDDK ALRILKNKRNQFECCDLTELAIEYENVE ALRILLNOFYNLFYRESSFELMFKKTRNLTIVKELLNOFRALINDNYGFPFINKBFK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TSLSLANELEFMEFILDNPILYSAPTTEPPPTPPPRESLFEALTQVKPIKQKGYQFIE
HNCTRFLUNSFKUIKKLIDLWVICNTENBRHAIISKIKADCSMETLLGLSSLYTRFYS
CEKESEINTKYLQGOLELIYANGKALLEFFIKDLKINFSKIFFNGGSMYNCEVIR
DTTTNEIIDFKYYVDDIYMDEQRNELYFNSILKCDIFFLKKIDSLDLASVDKTICLL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LKNGLPNMTNEDGMKVLAYLNDNGFKSFEVSGELCLFLRHFLINIII PPNFKLALOLF
SQTDINHRFLIYVFSLSFKSLRLFINSMDSISTITKLNITRHNNTEKSDEIFDIYQQIQ
YYCHDNGFIDIDNFIEILELFLKKFHXONNNNNNNNNNNNNNNNNGFESLEEDADT
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FSKYIINLPGIKVPIDIPNRGVLNGSEPSGNNSTHTVPGVNLPKCFNLNDFSFDYVIG
ENENHEKVGSPLDILNKLIESPSINLYNHAPSNNSKTSLKSDYPHDGPNYDLQPLLEI
RRVDSFPKYLQWIQLNCQHYQNIRNEQFTYNSPFHLKKPTKNDQIGSSSPPPPSHSTI
                                      RARLGTHTGFVNQLVTPYHVDIKCTVKSEISKEIVEETVAKASGKASMVLSDDAQSRG
SGGRMTSSYSSSSASTQGSNTTGKTFAGAGSKFTTPSAVPKSSGSTLGFDDEQQVRDT
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RGKFGDTHSLLIMLENDLLPLIKDKIKHGDHIEITYDSMLELFSKLSTEPSINSNKNK
NKYKDEDYLKIIELLMKHRRDEFEVFDLIMMAVSSRSPDVIRLLVNEPYSVIIYPTML
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QSDTQLYFKSALDQILLRIEEKSYEINSPFNENLENPFLESFIYGDIKTCNIILKYYP
NQFKITKDSITKTLEKEKINIIKYYYKVENCKNLINNFKNDNNLLKHLKNELLNHPMY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DNSEEEEEQEEEIDDKNGNNNNDNEEDENAHNHNNDNNEDIEPNDDDDNNNEDIEFYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GDDDNSDDDEMEIDDSRRLPLEMFFIQPNIQQILKSLVDQHLNSLISKRKNHLFKSSF
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FFVSFFQNEIYSFSLFYSREDLILFLIANYNIDIDLHPPLFKPDRGHSQYLECKFIFE
NTIILLGKGNGGVNELISNLQDNLVGYGLVRIVEKIDNSDTIKFAYINWIGEEIPRML
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MIKNENLMKHRVYQFNSPYESLLPTGTIFSNVKIIKKELPSPSTTTIESTFLKIDNFE
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                                                                                                                                                                                                                                                            /note="GeneID exon scores (in order of location ranges):
60.04 - GSCJ ID dd_02763"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      complement(13962. .16571)
/note="GeneID exon scores (in order of location ranges):
121.50 - GSCJ_ID dd_02764"
/codon_starts.
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17246. .21229
/note="GeneID exon scores (in order of location ranges):
207.54 - GSCJ_ID dd_02765"
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/bx xref="G1:28829242"
/tranel=til
                                                                                                                                                                                                                                               complement (12821. .13888)
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                                                                                                                                                                                                        TITQNSGTSSRVKA"
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CDS

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LYKKNLAVI ELLLKSFDNFNFIHQPEQMSAIVDKERNLFHISGELFQVDKKFSFQIIR
IIKLIMDKFNKLTKDQINIENISTTTYRLFLNYLYDQLLRVKGLTIDQLEYVRSIIPE
                                                                                                                                                                                                                                                                                                                                                                                                   KKYITQFDTILKELIKQLSFNICTNFSDRDEIVYELPSPSTTTTTIERTFLKIDNFEK
PIPNKSTIKVNMNSDKLIQLFKPISKLINSFKYSDGVMESICRVMNVNEIQRFIQYNF
CESFFQNEIYTYSVFFSRDDLMSFLLNNFNIDIDLHFPSFEFNRGYSQYLE"
                                                                                                                                                                                                                                                                                                                                       QLLNNNFETYRIFFYLNIRSSKLSNYLIKRPGITYFIRNSTELLYNNFYNTAEPITDE
IIGFDLRKYLNFELFTYDYILGRELNQYNNSGCSGCSGCSSSSSSSSSGGDDGRKNN
                                                                                                                                                                                                                                              translation="MIPNYDILIEFLSSVTNIIPPLELKISNIKEPLSGKLGTILLMQ"
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/note="GeneID exon scores (in order of location ranges):
52.65, 16.37 - GSCJ_ID dd_02766"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bukaryota; Mycetozoa; Dictyosteliida; Dictyostelium.
1 (bases 1 to 5441)
Glockner,G., Bichinger,L., Szafranski,K., Pachebat,J., Dear,P.,
Lehmann,R., Baumgart,C., Parra,G., April,J.F., Guigo,R., Kumpf,K.,
Tunggal,B., Cox,E., Quail,M.A., Platzer,M., Rosenthal,A. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            join(23880. .23905,24093. .24438)
/note="GeneID exon scores (in order of location ranges):
-3.80, 10.29 - GSCJ_ID dd_03433"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 83
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Direct Submission
Submitted (04-MAR-2003) Genome Analysis, Institute of Molecular
Biotechnology, Beutenberstr. 11, Jena 07745, Germany
4 (bases 1 to 54441)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   144 TGAAAGCAACGCTTGAAAAAAGGAAAGTTAGCCCTATCGGGTATATTTTGGAAGTTGTAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TGATTTATATGCTGATTTATGGGTGATTTTGCTTCCTTCTTTATACTTTATATTTCCC
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AC115584.2 GI:28828280
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0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 36188;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 47.8; DB 3;
                                                                                                                                       /product="hypothetical protein"
/protein_id="AAL92378.2"
/db_xref="GI:28829243"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2.4;
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0; Mismatches
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Dictyostelium discoideum
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AC079354.
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                                                                                                                                                                                                                                                                                                              106738 ATTTACATCTGTAATTATGAGTGATTTTCCTTTCCTCTTTAGATTTTTGGAATTTCTCA 106797
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Submitted (09-JAN-2002) Department of Genetics, Washington University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, USA On Jan 9, 2002 this sequence version replaced gi:14550326.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRI 09-JAN-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Direct Submission
Submitted (28-AUG-2000) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St. Louis,
MO 63108, USA
4 (bases 1 to 162554)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NOTICE: This sequence may not represent the entire insert of this clone. It may be shorter because we only sequence overlapping clone sections once, or longer because we provide a small overlap between neighboring data submissions.
                                                                                                                                                                                                                                                                                                                                                      86 ATTTTTCT----TAAGCAAATATTTCTTTGCTAATCAATAAATTATCAAAAGAAAAAAA 141
                                                                                                                                                                                                                                                                            26 ATTTATATGCTGATTTATGGGTGATTTTGCTTCCTTCTTTATACTTTTATTTCCCAA 85
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalia, Butherla, Primates, Catarrhini, Hominidae, Homo. 1 (base) 1 to 12254) Sulston, J. E. and Waterston, R.
                                                                                                                                                                                                                                      Gaps
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AC079354
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Center code: WUGSC
                                                                                                                                                                                                Length 152336;
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Armstrong,J., Cotton,M., Hawkins,M. and Dignan,G.
The sequence of Homo sapiens BAC clone RP11-1145F21
Upublished (2001)
(2015)
(2016)
(2016)
(2016)
(2016)
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(2016)
(2016)
                                                                                                                                          855 others
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                                                                                                                                                                                              Score 47.8; DB pred, No. 2.2; 0; Mismatches
                                                                              /note="assembly_fragment"
119737. .152336
/note="assembly_fragment"
a 29398 c 27664 g 42706
'note="aBBembly_fragment
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    106858 AAGAAATTACTGCTTAATAA 106878
                                                                                                                                                                                                                                                                                                                                                                                                                                  142 ACTGAAAGCAACGCTTGAAAA 162
                          AC079354.4 GI:18098550
                                                                                                                                                                                          9.0%;
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                                                                                                                                        51773
                                                                                                      misc_feature
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ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
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ORIGIN
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TITLE
JOURNAL
MEDLINE
PUBMED
REFERENCE
AUTHORS
TITLE
JOURNAL
REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AUTHORS
TITLE
JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REFERENCE
AUTHORS
                                                                                                                                                                                                                                      Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AC079354
LOCUS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          REFERENCE
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all regions were double stranded, sequenced with an alternate chemistry, or covered by high quality data (1.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by sequence from more than one subclone; and the assembly was confirmed by restriction digest. this sequence was finished as follows unless otherwise noted:

## MAPPING INFORMATION:

Mapping information for this clone was provided by Dr. John D. McPherson, Department of Genetics, Washington University, St. Louis MC. For additional information about the map position of this sequence, see http://genome.wustl.edu/gsc

## SOURCE INFORMATION:

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SUGKEL INFORMATION:
The RPCI-11 human BAC library was made from the blood of one male donor, as described by Osoegawa, K., Woon, P.Y., Zhao, B., Frengen, E., Tateno, M., Catanese, J.J. and de Jong, P.J. (1998) An improved approach for construction of bacterial artificial chromosome libraries. Genomics 51:1-8 The clone may be obtained either from Research Genetics, Inc. (http://www.resgen.com) or Pieter de Jong and coworkers at the Roswell Park Cancer Institute (http://bacpac.med.buffalo.edu)
VECTOR: DBACe3.6
NEIGHBORING SEQUENCE INFORMATION:
The clone sequenced to the left is RP11-107N15, 2000 bp overlap; the clone sequenced to the right is RP11-68666. Actual start of this clone is at base position 1 of RP11-1145F21; actual end is at

this clone is at base position 1 of RI base position 162554 of RP11-1145F21.

Data from AC069148 and AC064836 was used to finish this clone,

Location/Qualifiers 1. .162554 /organism="Homo sapiens" /mol type="genomic DNA'
/db xref="taxon:9606"
/chromosome="2"
/map="2" clone="RP11-1145F21"

/clone lib="RPCI-11" 329. 433 /rpt family="MIR" 1453. 1493

/rpt\_family="(CA)n" 1668. .1775

/rpc\_family="MIR" 1844. .1916 /rpc\_family="L1" /rpc\_family="L1" /rpcte="gimilar to EST BB614631 (NID:g15395798)"

2583. .2603 /rpt\_family="AT\_rich" 3403. .3542

3403. .3542 /rpt\_family="L1" 3568. .3595 /rpt\_family="AT\_rich" 3607. .4123

/rpt\_family="(GGAA)n" 4608. .5023 /rpt\_family="MaLR" 5049. .5224 Jou7. .4123 /rpc\_family="ERVL" /423. .4588

5049. .5224 note="eimilar to EST BB614631 (NID:g15395798)" 5692. .5991 /rpt\_family="Alu" 5973. .6004

5973. .6004 /rpt\_family="AT\_rich" 6261. .6476 /rpt\_family="MIR" 7016. .7295

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------ Genome Center
Center: Whitehead Institute/ MIT Center for Genome Research
                                                                                                                                                                                                                                            On Apr 13, 2000 this sequence version replaced gi:5932616. All repeats were identified using RepeatMasKer: Smit, A.F.A. & Green, P. (1996-1997) http://ftp.genome.washington.edu/RM/RepeatMasKer.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   contig of 7214 bp in length sign of 100 bp contig of 18346 bp in length contig of 18295 bp in length contig of 18295 bp in length sign of 100 bp contig of 28139 bp in length contig of 28139 bp in length contig of 32820 bp in length
                                                                                                                                                             Web site: http://www-seq.wi.mit.edu
Contact: sequence_submissions@genome.wi.mit.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          gap of 100 bp
contig of 32600 bp in length.
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contig of 5484 bp in length
gap of 100 bp
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gap of 100 bp
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contig of 5000 bp in length
gap of 100 bp
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/clone_lib="RPCI-11 Human Male_BAC"
1. .3638
                                                                                                                                                                                                       ----- Project Information
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        9323. .14322
/note="assembly_fragment"
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clone_end:SP6
vector_side:left"
3739. .9222
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     organism="Homo sapiens"
                                                                                                                                                                                                                         Center project name: L1752
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /mol_type="genomic_DNi
/db_xref="taxon:9606"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Location/Qualifiers
                                                                                                                                          Center code: WIBR
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119637
119737
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    COMMENT
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                                                                                                                                                                                                                                                                                                                                    FAGKQLEDGRTLSDYNIQKESTLHLVIALRGGGGKKKKKTYATPRVLKRKLRRVCLA
VLKYYKFDENGKTKRVLREDFBTCGAGVFRAQHARDROGYGKKTSTTLVKKSK"
join (22549 . 22739, 22926 . 23338, 23313 . 23554, 23119 . 24079)
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12.12, 21.76, 19.58, 31.39 - GSCJ_ID dd_0025s"
/codon_start=1
/product="similar to Homo sapiens (Human). GDP-fucose
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NSLESLHIGGECKENGEVMEFSQRKQRŠIKLSNAFVKEFGSMISSIAPLRKLSILGLN
SDQLIRYISSINKKIIKYFHVESIMDDGSYAHDDTPTIQSILVDNPQITDLKHTKFVF
TVQKQLFNDLYNGNEPFNTNVLNDLLSFKENVIFLYKK"
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                    FSFSICLDKFIYFLNKILNIDDINNIDSNNNNNNHNKIKKNKRYDMVEKLIMKQINQ
VRRNKKSNNQCNKDEDDSDSDSDSDSDESDDMDIDDSDESDDDDNNNDDCNKIIKCTCH
SLIFSKTNINYYNNSEFNDSMEDEKFNQEGIEEDEDEAKEIRVFRNEWLHFRSIIENH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
                                                                                                                                                                                                                                              /produčt="hypothetical protein"
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/db_xref="G1:288.289"
/t_anslation="MQIPIKTLTGKTITLEVEGSDNIENVKAKIQDKEGIPPDQQRLI
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/note="GeneID exon scores (in order of location ranges):
54.15, -0.85 - GSCJ_ID dd_00253"
/codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     27 ITTATATGCCGATTTATGCCTGATTTTGCTTCCTTCTTTATACTTTTATTTTCCCAAA 86
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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Submitted (27-AUG-1999) Whitehead Institute/MIT Center for Genome
Research, 320 Charles Street, Cambridge, MA 02141, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ő
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 9.0%; Score 47.8; DB 3; Length 54441; Best Local Similarity 63.5%; Pred. No. 2.3; Matches 73; Conservative 0; Mismatches 42; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Birren, B., Linton, L., Nusbaum, C. and Lander, B. Homo sapiens chromosome 4, clone RP11-363G1 Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /protein id="AAO50954.1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            HTG; HTGS PHASE1; HTGS DRAFT. HOmo sapiens (human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               transporter 1"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          VERSION
KEYWORDS
SOURCE
ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DEFINITION
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AUTHORS
TITLE
JOURNAL
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AUTHORS
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repeat_region 2903729333 /note="AluJb repeat: matches 1299 of consensus" repeat_region 2988830195 /note="AluY repeat: matches 1308 of consensus" repeat_region 30289. 310801 /note="AluS repeat: matches 1311 of consensus"	region 3077831937 // / / / / / / / / / / / / / / / / /	repeat_tegion 3034031300 /note="MRESSA repeat: matches 10961470 of consensus" repeat region 3130731609	/note="AluSq repeat: matches 1303 of region 3160931902	/note="MER52A repeat: matches 294 of c _region 3197432054	/note="L2 repeat: matches 26062691 Or consensus 3219932315 / Manner 2006	art: marcines ovr// or compensus	/NOCe="LZ repeat: matches 49272550 of combeneus" repeat_region 33206 / / / / / / / / / / / / / / / / / / /	rat: matches -455 358 of	יייייייייייייייייייייייייייייייייייייי	. 1400 OI	<pre>/note="AluYa5 repeat: matches 1306 of consensus" 3573635873</pre>	<b>~</b> m	~~	/	Tegron		., _,		•	4 /	4/	4/	4/	4 /	42345. /note="	4 /	43060. /note="		repeat_region 4375443987 /note="117 copies 2 mer ta 76% conserved"	7 7 6	poeat	142 05 05	
true right end of clone RP11-317C20 is at 56073 in this sequence.  Location/Qualiflers  1182012  /organism="Homo sapiens" /mol_type="genomic DNA" /hol_type="genomic DNA"	/ub_xtelm_caxon:psuo= /chromosome="9" /map="q31.1-31.3" /jone="pp11-43710"	repeat region 24562511	/note="28 copies 2 mer aa 71% conses 26222787	matches 20196 of consensus"	Deat: matches 25662749 c		inserved"	Compenso	meer ved	epeat: matches 10219 of conse	/note="L1PA5 repeat: matches 60296145 of consensus" repeat_region 93919426			/note="LTS" /note="LTS" repeat: matches 718785 of consensus"	, _,	-		 1638716491 /note="FLAM_A repeat: matches 22127 of co			1958420420 /note="L1PA5 repeat: matches 5308614		repeat_region 2116422730 /note="THE1A-internal repeat: matches 11578 of		3354		/note="MERSA repeat: matches 15187 of consensus" repeat_region 2578425850	/note="MER5B repeat: matches 2613026262					repear_region 4009428/1/ /note="HSMAR1 repeat: matches 12641287 of consensus"

Gaps

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82212 TTTTTCTGCAATAAATGTATCTTCCATAATCAAAAATTATTTAAAGTAACTAAAACAA 82271
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On Dec 9, 2000 this sequence version replaced gi:11557924.
During sequence assembly data is compared from overlapping clones. Where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the variation may not be found in the sequence submission corresponding to the overlapping clone, as we submit sequences with only a small overlap as described above.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This sequence has been finished according to sequence map criteria as follows. An attempt is made to resolve all sequencing problems, such as compressions and repeats, but not necessarily within known amnotated repeat sequence elements. Where the sequence is amnotated repeat sequence elements. Where the sequence is ambiguous, there is an annotation using the 'unsure' feature key. The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases:

Emm., EMBL; Sw., SWISSPROT; Tr., TREMBL; Wp., WORNDEP; Information on the WORNPEP database can be found at http://www.sanger.ac.uk/Projects/C_legans/wormpep This sequence thtp://www.sanger.ac.uk/Projects/C_legans/wormpep This sequence chromosome 9, constructed by the Sanger Centre Chromosome 9 Mapping
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  linear PRI 16-DEC-2000
                                                                                                                                                                                                                                                                                                                                                                                          chromosome 9, constructed by the Sanger Centre Chromosome 9 Mapping Group. Further information can be found at http://www.anger.ac.uk/HGP/Chr9

RP11-413-10 is from the library RPCI-11.2 constructed by the group of Pieter de Jong. For further details see http://www.chori.org/bacpac/home.htm

WECTOR: PABACe3.6

This sequence is the entire insert of clone RP11-413C10 The true left end of clone RP11-31J20 is at 123231 in this sequence. The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 182012)
                                                                                                                                                                                                                                                                                                           26 ATTTATATGCTGATTTATGGGTGATTTTGCTTCCTTCTTTATACTTTTATTTTCCCAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              82272 GATGTAGACTAGTCCAATATGAAGTCTTGGTCTGGAGACTCTTCATTCTAA 82322
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          146 AAAGCAACGCTTGAAAAAAGGAAAGTTAGCCCTATCGGGTATATTTTGGAA 196
                                                                                                                                                                                                                             Length 162554;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Au359846 182012 bp DNA linear PRI Human DNA sequence from clone RP11-413C10 on chromosome 9g31.1.31.3, complete sequence.
                                                                                                                                                                                                                                                                     77; Indels
                                                                                                                                                                                                                             ch 9.0%; Score 47.8; DB 9; 11 Similarity 55.0%; Pred. No. 2.2; 94; Conservative 0; Mismatches 77;
                    AL359846
AL359846.11 GI:11611367
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        25897.
                                                                                                                                                                                                                             Query Match
Best Local Similarity
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14461. .14538
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15030. .15052
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17670. .17790
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20860...2100

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7.pt. family="MIR"

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IDGLDDLDEEMESLNTSISTALTAVPTPEEHITHANSNSPPSLHKNTSSTNSASSL
SERDNNDSVVSTPQPGKVTSTATITTKKQPALSKATLETTSGNNVYSSQPSQSQPQPY
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TQTVTTQINIGRTNTPNNNNNNTNSPKVVHGDDLDNLLNNLTSQVKDIDSTGPTSRG
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SSSSINNNNNS INGSNTPNNTS INSNCSSINSSKLKKSKKKSHSSGSIGNVVCYSDI EMD
RRACSSLLKKKKLEFRLTINDKS I YHFENLQOFLDERKVEERKR I VKLI RLCOTRTRLD
TFTI ESSNSVSNQELVHLITTELOGGGFLQVPCHLI KDSONNMRS EPFKMF ISKSFFSLG
BFVARMFESL I WAGPWENHR LOGRKOOSSKQRNPKP I FKLLDSRKSNLKEFWSKQMT I
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LRNLINSIPNSNYPNITNSMISKAIDSNRIDYLKYLYENGGBIKNNPSLLQHLKNQL
SKSYDYNCFLDWLN"
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LFQSNKKNQPIKIINEMLPTLPIITSNSLRFKNTYNIFQLLLSNLSSLSSSFQIYSTL
LECAIEPLQPNTLSILINSPNLPITQDFKNRSLTPTNLNSTSIKTIERKIELILSNPK
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VEKYTKEEDDDNDNDQPXFHIIINHERVLLEVKKVTHOVIKNIYNGISSSGSSS
SKMIIIDHSLYHVVPTFISIKSPLLARY IMSRPFIYSIFTDDDGTTPYVNCSDNPGHP
GYDIRKYLNLHVFTFDPILGKOPDTHISPDLLLEKLIDALSYKPMTDDESLLPTEBDY
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AGSVCSGCGKAVSGRCVDALDKKWHPEHFVCAPCMNPLAGGSYTANNGKPYCKGCHNK
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EFLCFSPLERAGSTVDTVWRQIGAQLQNFYSESLSMDLNSEBSSRNRKKIGGNBNS
GSLASSGNNTPVRQKKKKKQDQXQDVFSKEKEKEKEKEKEKEKETISPTTTTTTTAN
ANSINELSNSGGGNSSKKLNESSDSTQSDSTNRTYFNANANPNTNTSIRKKRKKKSGRGGN
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db xref="G1:21240656"
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FNWILKLLRKNNSSEVEVGVGLIALQSLLLKDDFRIFFNNIDGSALLLNILQALSTSSVN
I QLLYETIYAIWLLTYNKDIAAAYSGTGLVANLVQLVKTVAKEKIVRLSLSTLRNLLN
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FVRHHSRGKAIMTITNQTRYHGYDVKSNEEVKNQALFALQKMMINNWEYLNAK"
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SIRLDSNSVLDSNKVKDNGIDSSDYLTKNWAY IQIAMDQAIFGY FGLDYKLVINGQRY
PDPYVELWQKWINGRESVFKSAGSVFVSAALLIFTFRLVTELVVEKETKIREGMSIMG
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                                                                                                                                                                                                                                                               /trānalation="MGEKSSQLKTLLKKNLLLKSKSKCGICCEIVFPIIIVLLVFAIL
VLVQLFKPNYDLIKTTQFSNRINENNIIIYGGKAGSLAVEQKGVIDMMKFQLSNELNK
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/note="nort ID:dd_02724"
/codon_etart=1
/product="POTASSIUM_CHANNEL_REGULATORY_FACTOR"
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protein id="AAM44363.1"
db xref="GI:21240652"
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/db_xref="GI:21240654"
                                                                                                                                                                 /protein_id="AAM44362.1"
/db_xref="GI:21240651"
                    note="ORF_ID:dd_02705"
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AC123513 61052 bp DNA linear HTG 29-MAY-2002 Dictyostelium discoideum chromosome 2 map 2779865-2840915 strain AX4, *** SEQUENCING IN PROGRESS ***.
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                                                                                                                                                                                                                                                                                                                                                      61 TCTTTATACTTTTATTTATTCCCAAATTTTTCTTAAGCAAATATTTCTTTGCTAATCAAT 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AC123513.1 GI:21240650
HTG; HTGS PHASE2.
Dictyostellum discoideum
Dictyostellum discoideum
Bukaryota; Mycetozoa; Dictyostellida; Dictyostellum.

1 (bases I to 61022)
Gloeckner, G., Eichinger, L., Szafranski, K., Pachebat, J., Dear, P., Lehmann, R., Baumgart, C., Parra, G., April, J. F., Guigo, R., Kumpf, K., Tunggal, B., Cox, E., Quall, M.A., Platzer, M., Rosenthal, A. and
                                                                                                                                                                                                                                                                                                                                                                                               /codon_gtart=1
complement(join(1193. .1583,1653. .6117,6198. .6330))
                                                                                                                                                                                                                                                                                                              Gaps
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NOTE: This is a 'working draft' sequence.
This sequence will be replaced
by the finished sequence as soon as it is available and
the accession number will be preserved.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                                                                                                                                                                                                                                                             121 AAATTATCAAAAGAAAAAAAAACTGAAAGCAACGCTTGAAAAAAGGAAAG 170
                                                                                                                                                                                                                                                                  DB 3; Length 6457;
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                                                                                                                                                                                                                                                                                                           39; Indels
Deutsche Forschungsgemeinschaft (DFG)
Location/Qualifiers
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    . 6457
/organism="Dictyostelium discoideum"

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/mol_type="genomic DNA"
/strain="AX4"
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join(448. .628,705. .803,875.
/note="ORF_ID:dd_02708"
                                                                                                                                                                                                                                                                Score 47.6; DB
Pred. No. 2.8;
0; Mismatches
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                                                                                                                                                                                                 2765
                                                                                    /mol_type="genomic DNA"
/strain="AX4"
/db_xref="taxon:44689"
/chromosome="2"
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616 c 632 g
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Best Local Similarity 64.5%;
Matches 71; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                             141
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Gloeckner.G. Eichinger,L., Szafranski,K., Pachebat,J., Dear,P.,
Lehmann,R., Baumgart,C., Parra,G., April,J.F., Guigo,R., Kumpf,K.,
Tunggal,B., Cox,E., Quail,M.A., Platzer,M., Rosenthal,A. and
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of
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Biotechnology, Beutenberstr. 11, Jena 07745, Germany
4 (bases 1 to 6457)
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Submitted (12-MAR-2003) Genome Analysis, Institute of Molecular
                                                                                                                                                                                                                                                                                                                                                  26 ATTTATATGCTGATTTATGGGTGATTTTGCTTCCTTCTTTATACTTTTATATTTATCCCAA
                                                                                                                                                                                                                                                                                                                                                                                             83305 ATTTACATCTGTAATTATGAGTGATTTTCTTTCCTCCTTTAGATTTTTGGAATTTCTCA
                                                                                                                                                                                                                                                                                                           Gaps
                                                                                 /note="LIME repeat: matches 704. .839 of consensus" 4993. .50299 /note="MER2 repeat: matches 7. .345 of consensus" 50323 .50465 /note="LIME repeat: matches 870. .1017 of consensus" 50468 .50902 /note="LIR26 repeat: matches 142. .603 of consensus" /note="LIR26 repeat: matches 142. .603 of consensus"
  'note="AluJo repeat: matches 120. .287 of consensus"
                                             .503 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Biotechnology, Beutenberstr. 11, Jena 07745, Germany
On Mar 4, 2003 this sequence version replaced gi:20087118.
CDS predictions from GeneID do not necessarily reflect true
Purther Information is available from IMB Jena, Department o
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                                                                                                                                                                                                                                                              DB 9; Length 182012;
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and the Univerity Colonge, Institute for Biochemistry
(http://www.uni-koeln.de/dictyostelium/project.shtml
Funding
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                      49601. .49693
/note="L1ME repeat: matches 421.
                                                                                                                                                                                                                                                            9.0%; Score 47.8; DE 63.8%; Pred. No. 2.2; ive 0; Mismatches
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Dictyostelium discoideum
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                                                             .49947
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Matches 90; Conserv
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                      repeat_region
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Query Match
Best Local Similarity
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AC006280/c
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DEFINITION
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                                RQLNHTNSTSSLISKFNQIDTPSGINQGWKGGVVVQKKQDPVKKSLAIFEKE"
comptement (join(12465). .24844,24917. .25293,23414. .25489))
/note="GeneID exon scores (in order of location ranges):
22.64, 31.07, 2.50 - GSCI_ID dd_01626"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /translation="Wortleplusluliulgauctilgestymyqukyegusgstytty
ykynkuksulsphodeetdtsunddugefsaqlkfykaalsmdilafvulffsacym
GWAAFKEISPANQTKLKUSLMGATVELIIATFVVLGLPKASREDCEDYAKDSSLNYTG
SQUBMGGGDIYKKFIGSHTDEDGSKLSWGPTTAMIAIVUGLGIAFFNNIFVYGGPVF
RS"
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RKRLDEEKQLLKKKLEKATSANNANSLELKTQUDHLSNLNAELKKKADDSIFALBREIDK

AKRLDEEKQLLKKKLEKATSANNANNANNANNANSSSSEEELKLINQRLRCTI

CNDRQKNYVIAKCFHVFCKECIYSNIDTRKRRCPSCNRAFAETDVHQIYY"

complement (join (17020. 17639, 17916. 18480))

//note="GeneID exon scores (in order of location ranges):

18.66, 24.28 - GSCJ_ID dd_01628"
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KIHSPLNISHSTIPSFHIFFTIFFILFFLEVFVFTFTSNSLFSLIINISGGWGLISDFGKR
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DSFNLIFYLLIYIYHPCKSNILVKRLNSYYDDGDELSINQNQSQQKSIDEINLY
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/note="GeneID exon scores (in order of location ranges):
249.99, 106.06 - GSCJ_ID dd_03289"
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phosphoprotein (Dentin phosphophoryn) (DPP); Dentin
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NDLCPDCYQNQQFFNGNDNNQFYFNYIGKREFKDGLIPNCIVYLAMFQWENGRINLTO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                163443 bp DNA linear HTG 12-AUG-2000
Plasmodium falciparum chromosome 12 clone 3D7, *** SEQUENCING IN
PROGRESS ***.
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Hyman,R.W., Fung,B.L., Qin,F., Tamaki,T., Kurdi,O.B. and Davis,R.W.
Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         84 AAATTTTCTTAAGCAAATATTTCTTTGCTAATCAATAAATTATCAAAAGAAAAAAAC 143
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* NOTE: This is a "working draft" sequence. It currently consists of 1 contigs. Gaps between the contigs.

* NOTE: This is a "working draft" sequence. It currently consists of 1 contigs. Gaps between the contigs.

* are represented as runs of N. The order of the pieces is believed to be correct as given, however the sizes

* of the gaps between them are based on estimates that have provided by the submittor.

* This sequence will be replaced

* by the finished sequence as soon as it is available and

* the accession number will be preserved.

* This sequence will be preserved.

* This provided by the submittor.
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/note="GeneID exon scores (in order of location ranges):
24.05 - GSCJ_ID dd_01625"
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1 (bases 1 to 16343)
Hyman,R.W., Fung,E.L., Qin,F., Rowley,D., Mao,J., Tamaki,T.,
Kurdi,O.B., Conway,A.B. and Davis,R.W.
Plasmodium falciparum 3D7 chromosome 12
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                                                                                                                                                                                                                                                                    Score 47.6; DB 3; Length 136240;
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Plasmodium falciparum (malaria parasite P. falciparum)
Plasmodium falciparum
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/organiem="Plasmodium falciparum"
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57.3%; Pred. No. 2.5;
*ive 0; Mismatches
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EQRTPLILTQKSLTSKSLNNIAVTSTSDSDGIKPKFIYSEFFEEDDEDEGSDEESDED
DEDEESDEEYREEDGFNDLEDDEEDQNNSYVQDLTKQIEKHFSLNDEKKNNNNNNNSQ
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SNSLSSSTTGTSQPLSNITTTKPKQNGKTGTNKKGNSKSSSSTPTKPTVTKNRANSTC
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Dictyostelium discoideum
Libases I to 136240)
Gloeckner, G., Eichinger, L., Szafranski, K., Pachebat, J., Dear, P., Lehmann, R., Baumgart, C., Parra, G., April, J.F., Guigo, R., Kumpf, K., Tunggal, B., Cox, E., Quail, M.A., Platzer, M., Rosenthal, A., and
                                                                                                                                                                                                                                                                 83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence and analysis of chromosome 2 of Dictyostelium discoideum
Nature 418 (6893), 79-85 (2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Dictyostelium discoideum chromosome 2 map 2097701-2233941 strain AX4, complete sequence.
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Submitted (12-MAR-2003) Genome Analysis, Institute of Molecular
Biotechnology, Beutenberstr. 11, Jena 07745, Germany
On or before Mar 4, 2003 this sequence version replaced
gi:20042931, gi:20066187.
CDS predictions from GeneID do not necessarily reflect true genomether Information is available from IMB Jena, Department of
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and the Univerity Colonge, Institute for Biochemistry I
(http://www.uni-koeln.de/dictyostellum/project.shtml
Punding
                                                                                                                                                                                 DB 2; Length 61052;
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                                                                                                                                                                               Score 47.6; DE Pred. No. 2.6; 0; Mismatches
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KUNNERY IE IMPLADILSNETNSINDPDLVGIQRREDDAMKRAVKKTKANTTTSFD
DLQFAFYSNTSQKTKTNEI IKGII IKI CGGGKVUDTWTKKTDYLLILKFSDLKUDYKTFNDI
ISKABGLKI ICVESTWINDSCIKSKKLVDHTNALVQQKTAPVVAI FTNTTTATTATTTT
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TITMGSNYDDAISTFGKITSSCIEVSDYKEGKKLGPEELSHPFKLIPSQQSDHSIKF
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CNKLEI NNNGSI NVENNSKI NILAGGL I MKDKSQI YLANSNI EI NGDAMLANQSI FNTM
NNLDLFI SGSLHLADDSLFLLFDNNEWTI NGDLLLAGI SKLFVNDKSELSI YGDLKI N
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STIFNSDIVVVIIDSVFKSHSLTVNNKSSLAI (DNSIIYSDDLIINEBEETHFTYVY
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NNNSTFEINQNGIYNLSSGGIYYTNDTNIKSNNITLKNDGIFNIDNDNVEINISFINN
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nlilpqnramkyrveeqkieindreqkikqlnykihqykenisclcrvmdqlnsgldl
linrydfenamdnilpkdnitesfeflssyitepytldekytldqslqkkyqktqstf
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EKVPTKDDSLLLSNGGNLLIDYDEICSSEYFTINNGSFYLYGQYSVYDSMDINRGSFI
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Anote="GeneID exon scores (in order of location ranges):
223.19 - GSCJ_ID dd_03123"
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protein FLJ12238"
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/note="GeneID exon scores (in order of location ranges)
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organism="Dictyostelium discoideum"
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Agency : Deutsche Forschungsgemeinschaft (DFG)

Location/Qualifiers

FEATURES

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7.1"
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Best Local Similarity 52.0%;
Matches 104; Conservative
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Plasmodium falciparum 3D7

Elasmodium falciparum 3D7

Blasmodium falciparum 3D7

Elakaryora, Alveolata; Apicomplexa; Haemosporida; Plasmodium.

Elakaryora, Alveolata; Apicomplexa; Haemosporida; Plasmodium.

Elakaryora, Alveolata; Alveng, E., White, O., Berriman, M., Hyman, R.W., Carlton, J.W., Pali, A., Nelson, K.E., Rowman, S., Paulsen, J.T., James, K., Eisen, J.A., Rutharford, K., Salzberg, S.L., Craig, A., Ryes, S., Chan, M.-S., Nene, V., Shallom, S.J., Suh, B., Peterson, J., Mather, M.W., Vaidya, A.B., Martin, D.M.A., Fairlamb, A.H., Praunholz, M.J., Roos, D.S., Ralph, S.A., McRadden, G.I., Cummings, L.M., Subramanian, G.M., Mungall, C., Veneer, J.C., Carucci, D.J., Hoffman, S.L., Newbold, C., Davis, R.W., Frasser, C.M. and Barrell, B.
INV 07-0CT-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Genome sequence of the human malaria parasite Plasmodium falciparum
Nature 419 (6906), 498-511 (2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Direct Submission
Submitted (13-58P-2002) The Institute for Genomic Research, 9712
Medical Center Dr., Rockville, MD 20850, USA
Location/Qualifiers
                                                                   146 AAAGCAACGCTTGAAAAAAGGAAAGTTAGCCCTATCGGGTATATTTTGGAAGTTGTAAAA
                                                                                                                                                                                                                                                                                                                  AE014830 250029 bp DNA linear INV 07-OC
Plasmodium falciparum 3D7 chromosome 10 section 2 of 7 of the
                                                                                                                                                                                                    206 TACTACRIGITCTCTAAGICCCACTCCTCTGTTTTCTTT 247
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/rpt_type=tandem
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1240. 1274
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1435.1483
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945. .1024
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289. .1319
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AE014830 AE014185
AE014830.1 GI:23494922
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By Hyman, R.W., Qin, F., Fung, E.L., Conway, A.B. and Davis, R.W. Direct Submission

L. Submission

Submission

Center, Stanford University, 855 California Avenue, Palo Alto, CA 94304, USA

On Apr 2, 1999 this sequence version replaced gi:4337173.

* NOTE: This is a "working draft' sequence. It currently consists of 3 contigs. The true order of the pieces a sorting. The true order of the pieces arbitrary. Gaps between the contigs are represented as * arbitrary. Gaps between the contigs are represented as * runs of N, but the exact sizes of the gaps are unknown.

* This record will be updated with the finished sequence as soon as it is available and the accession number will * be preserved.
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    (bases 1 to 196149)
    Hyman, R.W., Fung, E.L., Qin, F., Tamaki, T., Kurdi, O.B., Conway, A.B. and Davis, R.W.

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Plasmodium falciparum chromosome 12, *** SEQUENCING IN PROGRESS
                                            AAAGCAACGCTTGAAAAAAGGAAAGTTAGCCCTATCGGGTATATTTTGGAAGTTGTAAAA
  Gaps
  ö
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HTG. HTGS. PHASEL.
Plasmodium falciparum (malaria parasite P. falciparum)
Plasmodium falciparum
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47831: gap of unknown length
179129: contig of 131298 bp in length
179529: gap of unknown length
196149: contig of 16820 bp in length.
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Mismatches 109; Indels
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Unpublished
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/db_xref="taxon:5833"
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KTHSGLISTRGKONGELOKRYKODAKKNPYQLREDWWDANRHTWBAITCGAGGEDKY
FRQTACGTGTPTHKOCRCDDKANVDPTYFDYYPQYLAWFEBAABFCRKKNKKLKDV
KTNCRDGSGTGTPTHKOCRCDDKANVDPTYFDYYPQYLAWFEBABFCRKKKNKKLKDV
KTNCRDGSGASCGASCGASCRASRKTRAATIKYEGYEKKFYBERKKNYGTBU
GLLANBKACKDINEEKEKIDFTKNVEDDKNINKEGTFYHSQYCQPCGCGKKYTKNGN
GWEEKDYDGONIKLYKPTSAKFTEIKLKSGERHDDIKERIBQKTCNGSDGSGG
NSEKKELYDBKKCYQTGGLTKOOGCGWDDPDYDRLUSTGGCCILENOKKKESDPKS
ONEPEQFQKTFNEFFYFHIGRFLANDSMYWRGKVNSCINKSKREKCEEECKKECECFQK
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AKSGDTTGGKDGATGKSDGSICVPPRRRRLYIQKLHDWAEKVGDTATQPQVDTPSQSD
KLRDAFIESAAVETFFLWHRYKKIKDKEKLEEQQRQRENGELPGLSSSGDGDSNDPQS
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STSYFSNSGTTPIPPWRESVTTPQTWWELHGPHI WIGHLTGLYFKENGTDKPBYDTA
VRAQLWDSGKNTPQNSKYQTRVYCEEEESGRAK INI PDTSGDNTPTLANTPTLKRFVEI
PTFFRWLHEWGSDFCRQRKRMLKNVKHNÇRNI ERGGHEY CGGDGHDCTRDGI QHNNML
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RSPDQFLTSLKHCKNNEGDGSDPKNKIDFKEPLKTFGPLEYCKTCPPNKVNCNGPSRR
SGGNDQCTAVNGNEWEKIFSENGGNSTIDVHMIDRRGPYMEKKSQKLENSENPLFKT
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LKKRKI I EKCTQKGEKTCDDESKNDCACVKKWVEKKTTEWEQI KEHFKNRNQKDGDGN
DMKSSVRQLLDPLI YRMDLANGKGKI NELKEFLKSYECKCVDNAGNSEKDVVECLLQK
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ETCDKAADEKVEETVAQNEENNI PPAGPAPPADSPPAGPATDSGKENVVPEPPAPAAP
BSPPI PPLATSTLAMSVGI GFAAFTYFYLKKKTKASVGNLFQILQI PKSDYDI PTLKS
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MLONOPKDVPNDYSSGDIPPRYQPNTLYFDNNOEKPFITSIHDRNLYTGEEYSYNVNM
VNNDNIPINRDNNPYSGIDLINDSLNSNKVDIYDELLKRKENELFGTEHHPKHTNIYN
                                                                                                                                                                                 /codon_start=1
/product="erythrocyte membrane protein 1 (PfEMP1)"
/protein_id="AAN36275.1"
/db_xref="G1:234575.1"
/tb_xref="G1:23457575.1"
/tb_xref="G1:2345757575.1"
/translation="MYAAAKGGGSSQDAKHVLDEIGKDVYETVEKDAKIYKEALKGNL
OHAKGMGERASSNKTCTLVKEYYEHFNGDANSNRYPCKELSGKMGENRFSDTLGGGCT
                                                                                                                                                                                                                                                                                                                                                                                                    NKKI EGNKNNCGACAPYRRLHLCHHNLESI DTTSTTSDTLLAEVCYAAKFEGETLTTQ
HGQHQQTNPGTASQLCTVLARSFADI GDI VRGKDLFLGNDEEKKKRDELEENLQKI FA
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KEKGINKILDBEKKREEBERADGYVGYASGGONÓNNTTIDKLDHEDRODATKSKYG
EPTKPASKPEDLARGSGASPDTPREDSPPADLDDEEHDBDDEDDDAEEBEBEKKEE
BEEHKEEENBAAPEEKKEEGSSSPEEVEEKAKEAPAGPDACNIVQTLFSSIDKFSDDC
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/locus_tag="PFL0935c"
complement(join(11613, 12941,13715, 19156))
/locus tag="PFL0935c"
/nocus=THMMPfam hit to PP03011, Plasmodium falciparum
erythrocyte membrane protein (PFEMP), score 1.3e-56"
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17pt type=tandem

17pt type=tandem

17pt type=tandem

16563. .15614

/rpt type=tandem

17pt type=tandem

17pt type=tandem

/rpt type=tandem

17pt type=tandem

1915. .17943
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/rpt_type=tandem
12960. .13070
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12966. .13039
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13048. .13072
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9334. .19422
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20141. .20273
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20940..21079
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Pred. No. 2.8;
0; Mismatches 91; Indels 0;
Length 252650;
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Diagnosis of diseases associated with the immune system
Patent: WO 0200928-A 2148 03-JAN-2002;
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Sequence 2148 from Patent WO0200928.
AX347077
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Continuation (Z of 4) of PFMALIP2
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Best Local Similarity 52.8
Matches 102, Conservative
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Best Local Similarity 50.9
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AX347077/c
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JOURNAL
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PFMAL1P2 1
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CLYSCEKKLAIQTISGFIGCSCSFVPDNLDMKPLPCPVEKKKNSTISRLHLMDIYTNKT
ELTIPYKIVKEINLINDEPIYISLATLQQVIYIVVTGYSVYVFDEGTLSLIVKE
KISEDNI PICCDSKNORGIYANNKKGI IFY TITNYFNLINHLKLSNLBFKDKI IKNLC
VKYSYPGCDYISAYKKCINDMDFKKASKI ICLMKNYKIFEERISNNI AESILINMRKNI
PIRIIPPLERAYKQULNSFKSFKNTSQQSPLLLYSSYLLLEYDKLAYTSTELVKPVLQ
KKKEYLEKMIKDDKITCSEELGDLKYVLDLBELALNIY ELCSSHUKILSTYCLLMFNN
VLSYINNFKQINFDYVGIFIINNYEFPQGNADNKDSAFVGDFNSGSKNETMDFFNDG
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KKLOSKULESROSI ELWKVYLDETNYKKNYUDQY (165TLESNNADEITYTYKRAYID
KKLSSEL ELLEKY VILHNSE PSDIKNLONLI LITAIKSDSKKYWEY INKLDNYSGPOJ
AAVAYEYKLREBAFVIYKKENCYTSAI SVLLDKI LYNKNOKNNFHEFSSHDSTVPYY
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LLDYLKENKAEHKNLQTKLPERNIYNNVQVAETLEQMDIPTYYDKNKAAYLCEBKGL
YQRALENYTNINDIKYJIKKSTCFQKGGNNNNTTTTTTTSNMGDGHPDMNNSKGKI
SIEWIKNYFSTLSDSVCEELLEDFPKGSKINNEVVISICVQYYDKIGIKKIINKFPEN
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QYSYFANLALGEDVHYIMFKYIBACVKINNIQELDRICKDNAKXNPBGYRKELACK
LSDPRPLIYVCDIHYYIEGLASYYIKONSLLKYIEVYIKVNRNNAHKVIGVLDLDAS
EDFLLANLANNIKNISNIGNLIEIAEKRNRLKLLLPWLESRANEGYENIELHNALAKIY
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VYIDFYIEBEHLMIYMLLKILENKIINNRLVQTKKSNNNLAPLQKYEDIQAQNITAV
NETLAEIYLQNDDVIISLRNSIDEYDNFNQYPLLMKLENHKLEEMRRIAALLYKGNKKY
KEAINLSKKEKQYKDAIEIARVSKNNVYIEDLINYFIESKNKEAFCACLIVCYDLLKP
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NNQFNYSLNNNLSIMPPQNNFMSSNSFDKYDMFNNNTHF"
3056. .3105
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LKLKEYALAIEAAKKAKSLKTWKEVNPICVKYKQLKYAHTAGLQLIMHADHLDEIIKI
YEKKKYINELMNLLENGLNNERAHVGIYTELGILYAKYKPEKLMEPIRNYTNKMYTRK
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/translation="MSQNNPLSVCVADNLINYDIQNESFRLGNVSVEGDKYICVKENV
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KI CSLALNENEYMNYWKWI NNDTI AI VCEKNVYHWN I DI HNTKKNKDNDNNNNNNNNNN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /locus tag="PFL0930w"
/note="HWMPfam hit to PF00637, 7-fold repeat in Clathrin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /rpt_type=tandem
complement(<11613...>19156)
Complement(10915c"
complement(join(<11613...12941,13715...>19156))
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          'product="clathrin heavy chain, putative"
'protein id="AAN36274.1"
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608. .8601
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1440. 1476
1/rpt_type=tandem
1/758. 1801
1907. 1971
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2150. .2184
/rpt_type=tandem
2301. .2344
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8613. .8642
/rpt_type=tandem
8716. .8742
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2484. .2513
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                                                 Plasmodium falciparum 3D7

Bukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.

1. (bases I to 25256)

3. (bases I to 25256)

Gardner, M.J., Hall, N., Fung. B., White, O., Berriman, M., Hyman, R.W., James, K., Eslen, J.A., Rutherford, K., Salzberg, S.L., Cralg, A., Ryes, S., Chan, M.S., Nene, V., Shallom, S.J., Suh, B., Peterson, J., Angiuoli, S., Pertea, M., Allen, J., Selengut, J., Haft, D., Mather, M.W., Vaidya, A.B., Martin, D.W., Fairlamb, A.H., Fraunholz, M.J., Roos, D.S., Ralph, S.A., McFadden, G.I., Cummings, L.M., Subramanian, G.M., Mungall, C., Venter, J.C., Carucci, D.J., Hoffman, S.L., Newbold, C., Davis, R.W., Fraser, C.M. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Direct Submission
Submitted (29-JAN-2003) Stanford Genome Technology Center, Stanford
University, 855 California Avenue, Palo Alto, CA 94304, USA
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Hyman, R.W., Fung, E., Conway, A., Kurdi, O., Mao, J., Miranda, M., Nakao, B., Rowley, D., Tamaki, T., Wang, F. and Davis, R.W.
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Nature 419 (6906), 498-511 (2002)
                                                                                                                                                                                                                             203
                                                                                                              84 AAATTTTTCTTAAGCAAATATTTCTTTGCTAATCAATAAATTATCAAAAGAAAAAAAC 143
  24 IGATITATATGCTGATITATGGGTGATITITGCTTCCTTCTTTATACTTTTATTATTCCC 83
                                                                                                                                                                                                                             144 TGAAAGCAACGCTTGAAAAAGGAAAGTTAGCCCTATCGGGTATATTTTGGAAGTTGTAA
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Nakao,B., Rowley,D., Tamaki,T., Wang,F. and Davis,R.W.
Direct Submission
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/isolate="3D7": 36329"
/db xref="taxon:36329"
/chromosome="12"
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1220. . 1250
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/rpt_type=tandem
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1331. .1363
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AE014847 AE014188
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9.0%; Score 47.4; DB 9; Length 176109;
  /rpt_family="Alu"
20898. .21735
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21736. .22031
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49690.
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1928. 1948.

1938. 1948.

/rpt_family="MIR"

19564. 20147

20436. .2073.
                                                                                                                 MAPPING INFORMATION:

The sequence of this clone was established as part of a mapping and sequence of this clone was established as part of ampping sequencing collaboration between the NHGRI Chromosome 7 Mapping Project (Exto D. Green, Director), John D. McPherson in the Department of Genetics (Washington University), and the Washington University Genome Sequencing Center. For additional information about the map position of this sequence, see http://www.nhgri.nih.gov/DIR/CTB/CHR7, send mailto:egreen@nhgri.nih.gov or see http://genome.wustl.edu/gsc
chemistry, or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by sequence from more than one subclone; and the assembly was confirmed by restriction digest.
                                                                                                                                                                                                                                                                                                                       SOURCE INFORMATION:
Clone CTA-250D13 is from a release of the human BAC library
CITB-HS-250D13 is from a release of the human sperm. See:
Shizuya et al., Proc. Natl. Acad. Sci. USA 89:8794-7 (1992); U-J.
Kim et al., Genomics 34:213-8 (1996). The clone is available from
VECTOR: pBeloabcli (http://www.resgen.com).
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The actual start of this clone is at base position 1 of RG250D13;
actual end is at 176109 of RG250D13.
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/clone=lb="CITB-HS-A"
5770. -5950
/note="similar to EST T97069 (NID:9735693) ye50f03.rl"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This clone contains STS 8WSS2794 (NID:g1113588) and 6WSS350 (NID:g484309).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /organism="Homo sapiens"
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/chromosome="7"
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7143. .17416
rpt_family="MER1_type"
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/note="similar to
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/rpc_family="MIR"
18853. .18989
/rpc_family="Alu"
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/note="similar to
14504. .14805
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15108. 15194
/rot_family="L2"
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4806. 15107
rpt family="Alu"
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rpt family="MIR"
5633. .15723
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5790. 1607.
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6787. .16890
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EST AW946860 (NID:98124633)" /rpc\_family="Alu"
4167. 41939
4167. 42493
42310. 4246"
42583. 42791
/rpc\_family="MER1\_type"
43575. 43952
43575. 44952
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26006. .26319
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6377. .26788
/rpt\_family="L2"
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/rpt\_family="L1"
25605..25729
/rpt\_family="L1" /rpt\_family="L2" /rpt\_family="L1" 34369. .34576 /rpt\_family="L2" 35613. .35812 44407. .44534 /rpt\_family="Alu" 44582. .44701 /rpt\_family="L2" 50136. .50338 /rpt\_family="L2" 'rpt\_family="MIR" rpt\_family="MIR" 0945. .30984 family="L2" .49883

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NOTICE: This sequence may not represent the entire insert of this clone. It may be shorter because we only sequence overlapping clone sections once, or longer because we provide a small overlap between neighboring data submissions.
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2 (bases 1 to 156060)
4 (bases 1 to 156060)

Direct Submission
Submitted (18-FEB-1998) Stanford DNA Sequencing and Technology
Center, Stanford University, 855 California Avenue, Palo Alto, 94304, USA
                 /note="chemically treated genomic DNA (Homo sapiens)"
1174 c 22520 g 54649 t
                                                                                                                               Gaps
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HTG; HTGS PHASEL.
Plasmodium falciparum (malaria parasite P. falciparum)
Plasmodium falciparum
Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
I (bases I to 156060)
Hyman, R. W., Fung, E. L., Olin, F., Rowley, D., Mao, J., Tamaki, T.,
Kurdi, O. B., Conway, A. B. and Davis, R. W.
Plasmodium falciparum 3D7 chromosome 12
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* NOTE: This is a 'working draft' sequence. It currently consists of 2 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as * runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence.
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                                                                                           Length 113515;
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/mol_type="genomic DNA"
/db_xref="taxon:5833"
                                                                                           DB 6;
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Pred. No. 2.8;
1; Mismatches
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/db xref="taxon:32630"
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/clone="3D7"
                                                                                     Query Match
Best Local Similarity 54.4%;
Matches 93; Conservative
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Sulston,J.E. and Waterston,R.
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Homo sapiens BAC clone CTA-250D13 from 7q31, complete sequence.
AC003992
                                                                                                                                                    159 AAAAAAGGAAAGTTAGCCCTATCGGGTATATTTTGGAAGTTGTAAAATACTACRTGTTCT
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Park Avenue, St. Louis,
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Contact: sapiens@watson.wustl.edu
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Genome Res. 8 (11), 1097-1108 (1998)
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University, 4444 Forest
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Direct Submission
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22714 GATAATICAATITICATITITICTIATITICTAAATTATITITATICTAAAGIGTTATITIAG 22655
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Hyman, R.W., Fung, E., Conway, A., Kurdi, O., Mao, J., Miranda, M., Nakao, B., Rowley, D., Tamaki, T., Wang, F. and Davis, R.W.

Direct Submission
Submitted (29-JAM-2003) Stanford Genome Technology Center, Stanford University, 855 California Avenue, Palo Alto, CA 94304, USA (Location/Qualifiers 1.250707)
/organism="Plasmodium falciparum 3D7"
/mol type="genomic DNA"
/isolate="3D7"
                                                                                                                                                                                                                                                                                                                                          Plasmodium falciparum 3D7

Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.

[daesa 1 to 250707)

[daesa 1 to 250707)

Carlton,J.M., Pall,N., Fung,E., White,O., Berriman,M., Hyman,R.W., James, K., Eisen,J.A., Rutherford,K., Salzberg,S.L., Cralg,A., Kyes,S., Chan,M.S., Nene,V., Shallon,S.J., Suh,B., Peterson,J., Maghool,S., Petrea,M., Allen,J., Selengut,J., Haft,D., Mather,M.W., Valdya,A.B., Martin,D.M., Fairlamb,A.H., Francholz,M.J., Roos,D.S., Ralph,S.A., McFadden,G.L., Cummings,L.M., Subramanian,G.M., Mungall,C., Venter,J.C., Carucci,D.J., Hoffman,S.L., Newbold,C., Davis,R.W., Fraser,C.M. and Barrell,B.
                                                                                 AE014848 250707 bp DNA linear INV 11-FEB-2003
Plasmodium falciparum 3D7 chromosome 12, section 5 of 9 of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Genome sequence of the human malaria parasite Plasmodium falciparum
Nature 119 (6906), 498-511 (2002)
                                                            2 (bases 1 to 250707)

Hyman,R.W., Fung,E., Conway,A., Kurdi,O., Mao,J., Miranda,M. Nakao,B., Rowley,D., Tamaki,T., Wang,F. and Davis,R.W.
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20268. .20570
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29065. 29261
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/rpt_family="L1"
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University School of Medicine, 4444 Forest Park Parkway, St. Louis,
MO 63108, USA
4 (bases 1 to 176379)
Waterston, R.H.
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Submitted (29-0cr-2002) Department of Genetics, Washington
University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, USA
On Nov 29, 2000 this sequence version replaced gi:9799860.
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Park Avenue, St. Louis, Missouri 63108, USA
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University School of Medicine, 4444 Forest Park Parkway, St. Louis,
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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                     Gaps
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Homo saplens BAC clone RP11-504020 from 2, complete sequence.
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The sequence of Homo sapiens BAC clone RP11-504020
Unpublished (2001)
                     Indels
                     26;
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Contact: sapiens@watson.wustl.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Toward a complete human genome sequence
Genome Res. 8 (11), 1097-1108 (1998)
                                                                                                                                                                17924 GAAATGAATTAAATTATGAATGGGAAAAA 17896
 Pred. No. 2.7;
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Center project name: H_NH0504020
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Sulston, J.E. and Waterston, R.
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Submitted (09-MAY-2001) Du
University, 4444 Forest Pi
6 (bases 1 to 176379)
Waterston, R.H.
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7 (bases 1 to 176379)
70.8%;
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Best Local Similarity 70.8
Matches 63; Conservative
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The clone sequenced to the left is RPI1-514D19; the clone sequenced to the right is RPI1-538A12. Actual start of this clone is at base position 1 of RPI1-504O20; actual end is at base position 176379 of RPI1-504O20.
                                                                                                           all regions were double stranded, sequenced with an alternate chemistry, or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by sequence from more than one subclone; and the assembly was confirmed by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 donor, as described by Osoegawa, K., Woon, P.Y., Zhao, B., Frengen, E. Tateno, M., Catanese, J.J. and de Jong, P.J. (1998) An improved approach for construction of bacterial artificial chromosome libraries. Genomics 51:1-8. The clone may be obtained either from Research Genetics, Inc. (http://www.resgen.com) or Pieter de Jong vBCTOR: pBACE3.6
clone sections once, or longer because we provide a small overlap between neighboring data submissions.
                                                                                                                                                                                                                                                                                                                MAPPING INFORMATION:
Mapping information for this clone was provided by Dr. John D.
McPherson, Department of Genetics, Washington University, St. I
MO. For additional information about the map position of this
sequence, see http://genome.wustl.edu/gsc
                                                                                      This sequence was finished as follows unless otherwise noted:
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722. 1042
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/rpt family="L1"
/rpt family="L1"
/rpt family="L1"
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/mol_type="genomic DNA"
/db_xref="taxon:9606"
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/rpt_family="MalR"
5699. .6006
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5224. .5561
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/rpt\_family="MER2\_type" 8470\_.8545 /rpt\_family="MER2\_type"

repeat\_region repeat\_region

NOTICE: This sequence may not represent the entire insert of this clone. It may be shorter because we only sequence overlapping

us-10-027-632-1.rge

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NUMNINNINSSSSSGKTOGINILINNSWINERLHTFSGYYSLNILNDEIKIERINKCOMEKN
JOINGAST, 5577,5689. 5787,5923. 6077,6189. 6743)
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/note="Similarity eg to C.elegans RNA-binding protein
/TR(018318) BLAST Score: 378, aum P(1) = 3.6=35; 374
identity in 297 as overlap; splicing conserved in P.
knowlesi and P. yoelli; Pfam: match to PF00076 rrm, RNA
recognition motif: (a.k.a. RRM, RBD, or RNP domain) Score
58.01, B-value 1.1e-20"
                          Direct Submission
Submitted (17-DEC-1998) P.falciparum Genome Sequencing Consortium,
The Sanger Centre, Wellcome Trust Genome Campus, Hinxton, Cambridge
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /notes "Similarity: to kinesin-related protein.
D.melanogaster kinesin-like protein 67A (TR:P91945) BLAST
Score: 664, sum P(2) = 1.9e-67; 28# identity in 707 as
overlap; Pfam: match to PP00225 kinesin (6.1e-86), Kinesin
motor domain Score 311.54 B-value 6.1e-86".
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AL010143 AL010189 AL010157 AL010160 AL010165 AL010169
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Nature 419 (6906), 527-531 (2002)
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PFMAL3P7
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DEFINITION
ACCESSION
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JOURNAL
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KEYWORDS
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EKYY FKININQFI I LIMVKLLSINVY EI VKK I NSLANNY TYLY I NNKS YVKKNKI I NNY FI

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99; Conservative
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Matches 99; Conserv
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YLSENGWERHENKKMKL II KYE IRATPIDI INI LINKCKEYNY INNNLYDDI INI INTRDN
YLSELLLISNS FIKLINGY PRETFYNY I FIHILKLCKLAMYNY IFLYKMNEMPELHRLY
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SDPLANDE FESYFKKGOSFLEKKYNENSEN ITNEGORILKKROBILLIKKROBILLIKKROBLIKINKROBLIKKONNYTHNOGHIKKNSCHLAN
NDDMSRGCYLKGOSYSKGOFFRQQUNNCINITNKOGHIKKNSOKILLKI ISKNYKKILIT
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LYLFFHYHFNSLNEQFLNNIFCTLNHKNMITIYHCNQVFSSTLLIGSNQLKYQKGVYN
ILDTSILNHLKEIYFNKHVDISLNDMKNIVDFVFYFNKSITGNVLKAEYRKIKVSNDK
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YNMMSIYTPFIAPKKCCNKKKPVYFFSNNSFCKIYLMKFSFNIRMFILIKQIVEYLLK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           a.k.a. RRM, RBD, or RNP domain), score 1.4e-13"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              YGYNKKYVGSVAYRLYKIVKMVYTMKGGYVYLHKPKQKIPKKK"
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1656. .. 2618
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KELYEKRENENIKKOLOGIKKUI KOVI KESINLELOHOILUKKKKKKKEKETYSDVM
BTRASHLI KELI EKKKKLI SKI DONNANNINKHI FKYI KITKOY INCHNOHILI INFFEN
I IYEKI KAREKLKKRAKKELI ISKI DONNANNINKHI FKYI ITANDI HIGHLIAKVI KOI
I LKYFLEONYFVLI IHGPOTHGL PIENNWKLILKINHI QOLMINASY IHNONESLIKOE
HVPFKSY INLLINKLIKONOKENYTY ITPYKPY POLICIAN SSY IHNONESLIKOE
SYPTYLEODELI YKKNONNYTY ITPYKPY POLICIAN SSY IHNONESLIKOE
DVTY FLEDNSLIV YN STRONESKYI INGNOLENENT I SKOTI EQOKI STFKOLCKSYA
SYPTYLEODELI YKKNONNYTY ITPYKRY POLICIANSY INSNELICO
KOYTY FLENYSLIVINOKATI FRINKCLI, HEKYLYKI I HILKYEDEKROPFI I CO
KSYNSFSDNLIKKYKI LULITOCHTI FRUNKCLI, HEKYLYKI I HILKYEDEKROPFI I CO
KSYNSFSDNLIKKYKI LULITOCHTI FRUNKCLI, HEKYLYKI I HILKYEDEKROPFI I CO
KSYNSFSDNLIKKYKI LULITOCHTI FRUNKCLI, HEKYLYKI I HILKYEDEKROPFI I CO
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KSYNSFSDNLIKKY SKKSPI KEI KNI CTFQCUS FMSCTYKNFTNNEENNFI I VSDNEI
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KXYETPSNAQSILLASLIDINKKKTYKKLANI NEKUI HSLEPYSSYTYD
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                                                                                                                           KYEKLYMSKVLFNNI EKRMI KRKI ENMDAKI KLANSFRHI NKYNKYVMNKFCKKWKKR
KYELLIKCHTAI SQY IDTNNIA I DILLYYTLTTITTY YYMNI CSQONNI KINSI SSFI ITYEKF
I I FI LINKOVLLKKEQI VNI NYYLYY YKONLCI HTLKYVHYKLYKSYYY ILAYWKEI I LIK
I LQRNKTFKNYMDFI HFNNNSRTSNNA I QNI EKNE I HKFNSTYMYLLANY PSI SQTSYK
KOTDISSILILFDFLSSYQIDEIMILARCIKMKGQIESSHMHEKRDLEEIHTNIMKNF
LYSQKLRGREEKMKYEVTSIMYNEKKKKKKKSSIKNIMKNPFVTLQLRKFEYISKIFKN
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SRQKYWGVNIPLKDIELDQNQKIIFNNQIMDVWFDSSVSYIYVLYMCKHILFHTYFNK
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IKREQIKNNI KHYTLNNNNNNDNNNNNNSI FSDDSLCFNNTSSI ETNSKRLPSHSYL
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10454. .10489
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /rpt_type=tandem
8579. 8620
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10342. 10382
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /rpt_type=tandem
7562. .7596
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<10873. .>16375
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Gaps

; 0

87; Indels

Length 250707;

DB 3;

Score 47.4; DE Pred. No. 2.7; 1; Mismatches

9.0%;



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/ trānslation="WKTRKLYGLLKKIYYEKRXDFFLYFFFLLIPFLLISFHLFLRNI
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KDFLSYAENDLIN FRLYNSEBDCLKYLKYAIBLKSEDFKNYNSLELNDDILNIHEND
KNSLLYNLHTNIINLKSSEPRINDLYKDYYTENBEBEN KRIKINRIHILKYVKNYBERYK
NFIKOLYKIKNBHYTOYRDDRKKLFTYNFYKNNYLYKTOKOYONFFLYYPOTAL
NVKFSYLFGLSPQSEGFKGKGLYKNAPLYNYYTENBYGYONFFLLYYPYYTTLSBKKKN
NVKFSYLFGLSPQSEGFKGKGLYKNAPLYNYYTENBYGYONFFLLYYPYYTTLSBKKYNYYYKKOX
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DOCKKNNNNNYYYYYNNDFGLITWYKYRISTGYRGYLLNNAULLTRRYDFRYBING
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NKREBITMEYKTTDEREYQVNNEYINENVGYDERGGKYKTTELKLNDFFIYKMYKYYYYYSWL
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LFFYNITIFFYNITIFLAGORYNNEYINENGTRENKTNIENFLCCLKINNYKID
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XYGLFIFFLESFRLITISGSSNYLLTFFYLLIPBESFCLSLDFIFFITIKNNYKID
XYGLFIFFLESFRLITISGSSNYLLTFFYLLITYFRKOMMANTKYRGKSKSITN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note="gynonym: PFC0875w"
join(10596. 10737,11044. .11146,11373. .20416,20578. .20690)
/gene="MAL3P7.4"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 join(10596. 10737,11044. 11146,11373. 20416,20578. 20690)
gene="MAL3P7.4"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /translation="MANTYDELYVPLSYYILQNEGGNTSKIDQANTKKPKKKEVINKS
SLIIDIKPYGENTDLDEVLKLVKNITMEGLTWGKAHKKTPFAFGLFKLQVSCVIVDDL
VNTDELIETIENLGLDNEQLQKKKQMDDDEENYDEDDEIGGLVQSAEIISFNKL"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /Jobe="Revised: added 3' exon, possibly spliced at 5' end, revised: added 2x 5' exons by similarity with P. knowlesi; signal anchor predicted by SignalP 2.0 HWM (Signal peptide probability 0.001, signal anchor probability 0.997) with produce site probability 0.000 between residues 36 and 37 Pfam match to entry PP00005 ABC_tran, ABC transporter, score 72.50, E-value 9e-18"
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NKSNEEKKKKLLIDEDELWALNFEKSIKKDIISPIGHDEKSRHNEGMKEEEEDEDDEDD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /Jone="Similarity to P. falciparum elongation factor
1-beta, (AAF27524) (276 aa), fasta scores: opt: 366, E():
11-15, 53.2% identity in 141 aa overlag, revised:
shortened exon 2, splicing confirmed in P. knowlesi; Pfam:
match to PF00736 EPIBD, EF-1 guanine nucleotide exchange
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ODEDDDDDDSVDIKYKRHKEKRKSLTTKKYDKKEKHKRKSDHRDXHRRRENHSRHREK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DIAVIKSGQI I FKGSKNS FQKLIEYKFTLNI QFNGLPNEEQTNYLSQEKIMSALNKKG
VIKSPRKVANNYVDGYNVGRI SSHESS INDKKKDNNDNNNDDDNNKNNSVDHIDHLFD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ILVTNINEFTNNRDI IKKNI IKFIKGTRNENKNCFIFPNENHIYCTYKINELESLKKL
LCVLNKFKNILLTYQLKTIDIYYTYIYIYTTNBKKKLLKNIQDKDIKYLIEIDPLFFLF
FQNFKYFNELNNLLLMKNNHMQPISYNFAYLRDILVRGNENKNIINSTNHDDNPYDIN
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/protein_id="CAB39068.2"
/db_xref="GI:8052274"
                                                                                                                                                                                                                                                                                                                                                                                          Join(7801. .7928,8084. .8234,8392. .8583)
                                                                                                                                                                                                                                                             EKDKKSHKRRHKHSYDKYSSRSRSYSTSSSTDR"
join(7801. .7928,8084. .8234,8392. .8583)
/gene="MAL3P7.3"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 domain Score 61.10, E-value 7.9e-22"
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/db_xref="G1:23477031"
/db_xref="COA:097278"
/db_xref="SPTREMBL:097278"
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gene

SGS

CDS

MYNNHNKYGKYKNNNNNSFYNMRDDTELTDIEENISSKKKKNKFIEKEFSYNTYRNN

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KNNDENDEYGEYDNYDDNMIMSNTSNIMKKKNIKKONIFKTCINFFTTYIKPTLLLKL
                                                                                                                                 158 GAAAAAAGGAAAGTTAGCCCTATCGGGTATATTTTGGAAGTTGTAAAATACTACRTGTT 216
                                                      Gaps
                 Length 253305;
                                     ö
                                   82; Indels
                  DB 3;
                 Score 47.4; DB Pred. No. 2.7; 1; Mismatches
                 similarity 53.6%;
                                    Conservative
                                  196
               Query Match
Best Local 8
                                    Matches
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Search completed: February 14, 2004, 16:11:49 Job time : 2730 secs

Title: Perfect score: Sequence:

OM nucleic

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Scoring table:

Searched:

Minimum DB Maximum DB

Database

481.6 434.2 368.6 60

000

Score

Result

443 120

9

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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 564)
Mahairas, G.G., Wallace, J.C., Smith, K., Swartzell, S., Holzman, T.,
Keller, A., Shaker, R., Furlong, J., Young, J., Zhao, S., Adams, M.D. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AQ790276 S64 bp DNA linear GSS 03-AUG-1999 HS_2240_Bl_ROI_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2240 Col=1 Row=L, genomic survey
                                                                                                                                                                         442 TCTTTATACTTTTATTTTATTCCCAAATTTTTATTAAGCAAATATTTCTTTGCTAATCAAT 383
                                                                                                                                                                                                    121 AAATTATCAAAAGAAAAAAAACTGAAAGCAACGCTTGAAAAAAGGAAAGTTAGCCC-TA 179
                                                                                                                                                                                                                    322 TCGGGTATATTTTGGAAGTTGTAAAATACTACGTGTTCTCTTCTAAGTCCCACTCCTCTG 263
                                                                                                                                                                                                                                                                                                                                    262 TITICITIGAGGAGGAAAGAGAAAGCAGTCACCTCTCTTCCATGACAACAACAACGAGAC 203
                                                                                                                                                                                                                                                                                                                                                                            300 CGGCTGCTTGCCTGCTCCATCACAGGAAGGTGCAGCAGAGGCCCTTTTCTTCCCAGGGTTG 359
                                                                                                                                                                                                                                                                                                                                                                                           202 CGGCTGCTTGCATCCATCACAGGAAGGTGCAGCCAGAGCCATTTTCTTCACAGGGTTG 143
                                                                                                                                                                                                                                                                                                                                                                                                                                  360 TGGCCACCTTGAACTATCCTGGCTTGCTAAGAAACTGCCCCAAGTGACGCACACTC 419
                                                                                                                                                                                                                                                                                                                   240 TITICITIGAGCAGGAAAGAGAAAGCAGTCACCCTCTTCCATGACAACAACCATGAC 299
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Contact: Mahairae GG, Wallace JC, Hood L
High Throughput Sequencing Center
High Throughput Sequencing Center
401 Queen Anne Avenue North, Seattle, WA 98109, USA
Tel: (206) 616-3618
Exa: (206) 616-3887
Email: jwallac@u.washington.edu
Clones may be purchased from Research Genetics (info@resgen.com).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         61 TCTTTATACTTTTATTCCCAAATTTTTCTTAAGCAAATATTTCTTTGCTAATCAAT
                                                                                                                                                                                                                                                            TCGGGTATATTTTGGAAGTTGTAAAATACTACRTGTTCTCTTCTAAGTCCCACTCCTCTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                   142 TGGGCACCTTGAACTATCCTGGCTTGCTAAGAAACTGCCCCCAAGTGACGCACTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence-tagged connectors: A sequence approach to mapping
                                                          1;
                         Score 481.6; DB 28; Length 515;
Pred. No. 3e-56;
1; Mismatches 5; Indels 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        scanning the human genome
Proc. Natl. Acad. Sci. U.S.A. 96 (17), 9739-9744 (1999)
99380589
                                                                                      1 CATGGTGATGCTGTAGTCGTGGCTGATTTATATGCTGATTTATGGGTGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 480 TCTCTGGTCAGGCCCAAGTCAC 501
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AQ790276
AQ790276.1 GI:5697900
GSS.
                            tch 91.0%; al Similarity 98.6%; 495; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens (human)
Homo sapiens
                             Query Match
Best Local Similarity
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AQ790276/c
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                                                        Matches
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COMMENT
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AUTHORS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Unpublished
Other GSSs: CIT-HSP-2005M18.TF
Contact: Mark Adams
Contact: Mark Adams
Contact: Mark Adams
Contact: Mark Adams
Contact: Mark Adams
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0200
Fax: 301 838 0200
Email: mdadams@tigr.org
Tel: 301 838 0200
Email: mdadams@tigr.org
Clones are available from Research Genetics (info@resgen.com). BAC
end search page:
http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html
Seg primer: M13 Reverse
Class: BAC ends.
           BM547682 AGENCOURT
AL551891 AL551891
BC02523 Home sapi
BC0390979 NISC_mq16
AL515321 AL515321
BX415058 BX415058
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AC032590 RXCT_23-2
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BX453223 BX46321
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhin; Hominidae; Homo.
1 (bases 1 to 515)
Adams, M.D., Rounsley, S.D., Field, C.E., Bass, S., Linher, K., Golden, Ak., Berry, K., Granger, D., Suh, E., Wible, C., Shizuya, H., Simon, M. and Venter, J.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Use of a random BAC End Sequence Database for Sequence-Ready Map
Building
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /cell_type="Sperm"
/clone_lib="CIT-HSP"
/note="Vector: pBeloBAC11; Site_1: HindIII; Site_2:
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                                                                                                                                                                                                                                                                                                                                                             ALIGNMENTS
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BC39079
AL515321
AL51523
BX415058
BX415058
ALS14047
CNS016CW
BX425800
BX425800
BX425107
BX46411
BM06326
BX46411
BM06326
BX46613
BX4637
AL514627
BQ925593
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /sex="Male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens (human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         102 C
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 Homo sapiens
 152
 ACCESSION
VERSION
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SOURCE
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B56032/c
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COMMENT
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us-10-027-632-1.rst

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Mahairas,G.G., Wallace,J.C., Smith,K., Swartzell,S., Holzman,T.,
Keller,A., Shaker,R., Furlong,J., Young,J., Zhao,S., Adams,M.D. and
Hood,L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        BX424950 1091 bp mRNA linear EST 15-MAY-2003
BX424950 Homo sapiens FLACENTA Homo sapiens cDNA clone CLOBA005ZA01
3-PRIME, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          196 AGTIGIAAAATACTACRIGITCICTICIAAGICCCACICCICTGTTTTGAGCAGGA 255
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  274
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          315
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CCATCACAGGAAGGTGCAGCAGAGCCCTTTTCTTCCCAGGGTTGTGGGCACCTTGAACTA 375
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  436 TCCAGAATAAACCAAACCAGCTGTATTACTGGTCTTTGACATCCTCTCTGGTCAGGCCA 495
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            213 CCATCACAGGAAGGTGCAGAGAGCCCTTTTCTTCCCAGGGTTGTGGGCACCTTGAACTA 154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  393 AAAAAAACTAAAACAACGCTGAAAAAGGAAAGTTAGCCCCTATCGGGTATATTTTGGA 334
                                                                                                                                                             Contact: Mahairas GG, Wallace JC, Hood L
High Throughput Sequencing Center
University of Washington
401 Queen Anne Avenue North, Seattle, WA 98109, USA
Tel: (206) 616-3618
Fax: (206) 616-3887
Email: jwallace@u.washington.edu
Clones may be purchased from Research Genetics (info@resgen.com).
BAC end Web Server: http://www.htsc.washington.edu
Clones may Bacver: http://www.htsc.washington.edu
Seq primer: M13 Reverse
Class: BAC ends
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      rccagaaraaaccaaacrarrracragrerrracacarcrrracragacaa 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /clone lib="CIT Approved Human Genomic Sperm Library D"
/note="Organ: sperm; Vector: pBeloBAC11; BAC Clones in
E-Coli DH108"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             256 AAGAGAAAGCAGTCACCTTCTTTCCATGACAACAACCCATGACGGGTGCTTGCCTTGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              376 TCCTGGCTTGCTAGCTAAGAAACTGCCCCAAGTGACGCACACCTCAAGCTGTTCGGGGACT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              153 TCCTGGCTTGCTAGCTAAGAAACTGCCCCAAGTGACGCACTCAAGCTGTTCGGGGACT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            136 AAAAAAACTGAAAGCAACGCTTGAAAAAAGGAAAGTTAGCCCTATCGGGTATATTTTGGA
                                                                   Sequence-tagged connectors: A sequence approach to mapping and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gapa
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                                                                             scanning the human genome
Proc. Natl. Acad. Sci. U.S.A. 96 (17), 9739-9744 (1999)
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/db_xref="taxon:9606"
/clone="Plate=2005 Col=18 Row=M"
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Location/Qualifiers
1. 395
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195 DNA linear GSS 09-AUG-1999
HS_2005_A2_G09_MR CIT Approved Human Genomic Sperm Library D Homo
sapiens genomic clone Plate=2005 Col=18 Row=W, genomic survey
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
1 (bases 1 to 395)
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                                                                                                                                                                                                                                    /clone_lib="CIT Approved Human Genomic Sperm Library D"
/note="Organ: sperm; Vector: pBeloBAC11; BAC Clones in
E-Coli DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               564 GGTGATTATGCTTCCTTCTTTATACTTTTTATTGATTCCCAAATTTTTCTTAAGCAGATAT
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  BAC end Web Server: http://www.htsc.washington.edu Plate: 2240 row: L column: 1 Seq primer: M13 Reverse Seq primer: M13 Reverse High quality sequence stop: 564.
                                                                                                                                                                                                                                                                                                              31 others
                                                                                                                                                                 /mol_type="genomic_DNA"
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/clone="Plate=2240 Col=1 Row=L"
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/organism="Homo sapiens"
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Matches 465; Conservative
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/clone lib="Homo sapiens PLACENTA"
/note="Vector: pCMVSPORT 6; lst strand cDNA was primed
with a NotI-olisq(dI) primer. Five prime end enriched,
double-strand cDNA was digested with Not I and cloned into
the Not I and ECORV sites of the pCMVSPORT 6 vector.
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                                                                         Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo. Li (bases 1 to 1091)
Li W. B., Gruber, C., Jessee, J. and Polayes, D. Full-length cDNA libraries and normalization
                                                                                                                                                                                                                                                                                                                                                ••
                                                                                                                                                                                                                                           Email: segref@genoscope.cns.Ir, Web : www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 6403.r For
more information about this cluster, see
http://www.genoscope.cns.fr/
cgi-bin/cluster.cgi?seq=CLOBA005ZA01FPl&cluster=6403.r. Contact :
Feng Liang Email : fliang@lifetech.com URL :
http://fulllength.invitrogen.com/ InvitroGen Corporation 1600
Faraday Avenue Genoscope sequence ID : CLOBA005ZA01FPl.
Location/Qualifiers
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Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     230 CACTCCTCTGTTTTCTTTGAGCAGGAAAGAGAAAGCAGTCACCCTCTCTTCCA 282
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         399 others
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Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         /organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CLOBA005ZA01"
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 GI:30770416
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                                       Homo sapiens (human)
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Best Local Similarity 30.5
Matches 71; Conservative
                                                             Homo sapiens
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/tissue_type="NEUROBLASTOMA"
/clone_lib="Homo sapiens NEUROBLASTOMA"
/clone_lib="Homo sapiens NEUROBLASTOMA"
/note="Vector: pCMVSPORT_6; lst strand cDNA was primed
with a NotI-oligo(dT) primer. Five prime end enriched,
double-strand cDNA was digested with Not I and cloned into
the Not I and EcorV sites of the pCMVSPORT 6 vector.
Library was not normalized."
library as 113 g 326 t 194 others
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Li, W.B., Gruber, C., Jessee, J., and Polayes, D.
Pull-length cDNA libraries and normalization
Unpublished
Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
BRail: seqref@genoscope.cns.fr, Web: www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 6537.f For
more information about this cluster, see
                                                                                                                                                                                                                                                                                                                         http://www.genoscope.cns.fr/
cgi-bin/cluster.cgiseq=CL0BB029ZG02FPl&cluster=6537.f. Contact
cgi-bin/cluster.cgiseq=CL0BB029ZG02FPl&cluster=6537.f. Contact
Feng Liang Email : fliang@lifetech.com/NL.
http://fulllength.invitrogen.com/ InvitroGen Corporation 1600
Faraday Avenue Genoscope sequence ID : CL0BB029ZG02FPl.
Location/Qualifiers
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AL514205 Homo sapiens NEUROBLASTOMA Homo sapiens CDNA clone CLOBB006ZG12 3-PRIME, mRNA sequence.
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Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: segref@genoscope.cns.fr, Web : www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
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Full-length cDNA libraries and normalization
Unpublished
On Feb 13, 2001 this sequence version replaced gi:12777699.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /mol_type="mRNA"
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/clone="CL0BB029ZG02"
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Homo sapiens
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Class: shotgun
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252 bp mRNA linear EST 15-MAY-2003
BX452020 Homo sapiens PLACENTA Homo sapiens cDNA clone CLOBA0072D06
BX425020
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BP 191 91006 EVRY cedax - France
BR 191 91006 EVRY cedax - France
BR 191 91006 EVRY cedax - France
BR 191 91006 EVRY cedax - France
BR 191 91006 EVRY cedax - France
BR 191 91006 EVRY cedax - France
Library was constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 8225.r For
http://www.genoscope.nn.fr/
cg1-bin/cluster.cg1?seq=CLOBA007ZD06FP1&cluster=8225.r. Contact :
Feng Liang Email : fliang@lifetech.com URL :
http://fulllength.invitrogen.com/ InVitroGen Corporation 1600
Faraday Avenue Genoscope sequence ID : CLOBA007ZD06FP1.
                                                                                                                                                                                                                                                                                                                                                                                                                 83
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Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.

    (bases 1 to 252)

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                                                                                                                                                                                                                                                                                                         145 others
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                                                                                                                                                                                                                                                                                                                                                                                52;
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                                                                                                                                                                                                                                                                                        Library was not normalized.
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/mol_type="mRNA"
/db_xref="taxon:9606"
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Contact: Genoscope
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/cissue type="PLACENTA"
/cione lib="Homo sapiens PLACENTA"
/clone lib="Homo sapiens PLACENTA"
/note="Vector: pCMVSPORT_6; lst strand cDNA was primed
with a NotI-ollygo(dT) primer. Five prime end enriched,
double-strand cDNA was digested with Not I and cloned into
the Not I and EcoRV sites of the pCMVSPORT 6 vector.
Library was not normalized."
35 others
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ENTOK14TR Entamoeba histolytica Sheared DNA Entamoeba histolytica
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Contact: Brendan J Loftus
Department of Bukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD.20850, USA
Tel: 301 838 5208
Exa: 301 838 3543
Email: bjloftus@tigr.org
Clones are derived from the Entamoeba histolytica HM1:IMSS sheared
                                                                                                                                                                                                                                                                                                                                                                                                                                                     65 TATACTTTTATTTATTCCCAAATTTTTCTTAAGCAAATATTTTCTTTGCTAATCAATAAAT 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Loftus, B., Wang, Z., Van Aken, S. and Praser, C. Determination of clone end sequences from Entamoeba histolytica HM1:1MSS sheared DNA library (2001)
                                                                                                                                                                                                                                                                                                                                                        5 GTGATGCTGTAGTCGTGGCTGATTTATATGCTGATTTATGGGTGATTTTGCTTCCTT
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                                                                                                                                                                                                                                                            Length 252;
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/mol_type="genomic DNA"
/strain="HM1:IMSS"
                                                                                                                                                                                                                                                         10.4%; Score 55; DB 13;
47.9%; Pred. No. 3.2e+02;
tive 23; Mismatches 63
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Eukaryota; Entamoebidae; Entamoeba.
1 (bases 1 to 894)
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BH137168
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High quality sequence stop: 522.
Location/Qualifiers
/clone="CL0BA0072D06"
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Matches 79, Conservative
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Homo sapiens
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/clone_lib="Homo sapiens PLACENTA"
/clone_lib="Homo sapiens PLACENTA"
/clone_lib="Homo sapiens PLACENTA"
/clone_lib="Homo sapiens PLACENTA"
//thote="Vector: pCMVSPORT 6; lst strand cDNA was grimed yith a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoRV sites of the pCMVSPORT 6 vector.
Library was not normalized." 88 others
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3-PRIME, mRNA sequence.
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Genoscope
Genoscope
Genoscope
- Centre National de Sequencage
BP 191 91006 EVRY cedex - Franch
Bmail: seqrefégenoscope.cns.fr, Web: www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Library was constructed by Life Technologies, a division of
Library was constructed by Life Technologies, a division of
Library was constructed by Life Technologies, a division of
Library was constructed by Life Technologies, a division of
Location (Company Avenue Genoscope sequence ID: CLOBA002ZH05FP1.
                                                                                                                                                                            86
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               whole genome shotgun sequencing projects. In Genome Sequencing: A Practical Approach, eds. M. Vaudin and Barell, Oxford University Press, 1999)."
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                                                                                                                                                                            Gaps
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                                                                                                          10.3%; Score 54.6; DB 28; Length 894; 52.9%; Pred. No. 1.9e+02;
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                                                                                                                                                                                                                                                                                                                                                                       247
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Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
Full-length CDNA libraries and normalization
                                                                                                                                                                                                                                                                                                                                                                     207 ACTACRIGITCTCTTCTAAGTCCCACTCCTCTGTTTTCTTT
                                                                                                                                            0; Mismatches 104;
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/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CLOBA002ZH05"
H.O. and Venter, J.C.
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Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
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Li W. B., Gruber, C., Jessee, J. and Polayes, D.
Full-length cDNA libraries and normalization
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Genoscope - Centre National de Sequencage
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Bmall: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
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/ Organism="Homo sapiens"
// Organism="Homo sapiens"
// Appe="mRNA"
// Clone="Laxon:9606"
// Lissue type="PLACENTA"
// Clone="Lype="Flow sapiens PLACENTA"
// Inote="Vector: porvSPORT 6; lst strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoRV sites of the pCMVSPORT 6 vector.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Contact: Genoscope
Contact: Genoscope
Contact: Genoscope
Contact: Genoscope
Benoscope - Centre National de Sequencage
BP 191 91006 EVRX cedex - France
Bmail: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 9703.f For
                                                                                                                                             Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 817.f For
more information about this cluster, see
                                                                                                                                                                                                                                                                                                                      http://www.genoscope.cns.fr/
cgi-bin/cluster.cgi?eeq=CLOBA007ZH01FP1&cluster=817.f. Contact
cgi-bin/cluster.cgi?eeq=CLOBA007ZH01FP1&cluster=817.f. Contact
Feng Liang Email : filang@lifetech.com URL :
http://fulllength.invitrogen.com/ InVitroGen Corporation 1600
Faraday Avenue Genoscope sequence ID : CLOBA007ZH01FP1.
Location/Qualifiers
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                                                                                                                           On Feb 13, 2001 this sequence version replaced gi:12777213
     Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
Full-length cDNA libraries and normalization
                    1 (bases 1 to 1162)
Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
Full-length cDNA libraries and normalization
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/organism="Homo sapiens"

/mol_type="mkNa"

/db xref="taxon:9606"

/clone="CL0BB015ZE10"

/clone="Lib="whomo sapiens NEUROBLASTOWA"

/clone="Vector: pCWVSPORT 6; lst strand cDNA was primed
/note="Vector: pCWVSPORT 6; lst strand cDNA was primed
with a Not1-oligo(dT) primer. Five prime end enriched,
double-strand cDNA was digested with Not I and cloned into
the Not I and EcoRV sites of the pCMVSPORT 6 vector.

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Li, W.B., Gruber, C., Jessee, J. and Polayes, D. Full-length cDNA libraries and normalization Unpublished
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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BP 191 91006 EVRY cedex - France
Bmali: sequefégenoscope.cns.fr, Web: www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 1606.r For
more information about this cluster, see
http://www.genoscope.cns.fr/
cgi-bin/cluster.cgi?seq=CL0BB015ZE10FP1&cluster=1606.r. Contact :
Feng Liang Email : fliang@lifetech.com URL :
http://fulllength.invitrogen.com/ InvitroGen Corporation 1600
Faraday Avenue Genoscope sequence ID : CL0BB015ZE10FP1.
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AL514791.2 GI:30464676
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/tissue type="PLACENTA"
/clone lib="Homo sapiens PLACENTA"
/clone lib="Homo sapiens PLACENTA"
/note="Vector: pCMVSPORT 6; lst strand cDNA was primed
with a NotI-oligo(dT) primer. Five prime end enriched,
double-strand cDNA was digested with Not I and cloned into
the Not I and EcoRV sites of the pCMVSPORT 6 vector.
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/clone lib="Homo sapiens PLACENTA"
/note="Vector: pCMVSPORT 6; lst strand cDNA was primed with a NotI-oligo(T) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoRV sites of the pCMVSPORT 6 vector.
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BX425020 Homo sapiens PLACENTA Homo sapiens cDNA clone CLOBA007ZD06
BX425020
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 252)
                                                                                                                                                                                                                                                                                                                                                                                        314 TTTTKGGGGGKGTTGTTTTTTTTTTTTTKGKKGKKKKDKTTTDTTATWWAWWWW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              72 TTATTTATTCCCAAATTTTTCTTAAGCAAATATTTCTTTGCTAATCAATAAATTATCAAA
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cgi-bin/cluster.cgi?seq=CLOBA007ZD06FP1&cluster=8225.r. Contac
cgi-bin/cluster.cgi?seq=CLOBA007ZD06FP1&cluster=8225.r. Contac
feng Liang Email: fliang@lifetech.com URL:
http://fulllength.invitrogen.com/ InvitroGen Corporation 1600
faraday Avenue Genoscope sequence ID: CLOBA007ZD06FP1.
Location/Qualifiers
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BP 191 91006 EVRY cedex - France
Email: seqref@genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 8225.r
more information about this cluster, see
                                                                                                                                                                                                                                                                                  10.0%; Score 52.8; DB 9; Length 1104; 36.7%; Pred. No. 3e+02; tive 46; Mismatches 54; Indels 0.
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265 c 143 g 154 t
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Best Local S:
Matches 58
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/clone lib="Homo sapiens PLACENTA"
/note="Vector: pCMVSPORT 6; lst strand cDNA was primed
/note="Vector: pCMVSPORT 6; lst strand cDNA was primed
with a NotI-callgo(dT) primer. Five prime end enriched,
double-strand cDNA was digested with Not I and cloned into
the Not I and EcoRV sites of the pCMVSPORT 6 vector.
Library was not normalized."
16 c others
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AL513809 Homo sapiens PLACENTA Homo sapiens cDNA clone CLOBA0092F09
3-FRIME, mRNA sequence.
AL513809
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Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
I (bases I to 1104)
Li, W. B., Gruber, C., Jessee, J. and Polayes, D.
Full-length cDNA libraries and normalization
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             27 ITTADADGCTGATTTATGGGTGATTTTGCTTCCTTTTATACTTTTATATTTCCCAAA 86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             On Feb. 13, 2001 this sequence version replaced gi:12777303.

Context: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invirogen. This sequence belongs to sequence cluster 1095.f For more information about this cluster, see
                  http://www.genoscope.ons.fr/
cgi-bin/cluster.cgi?eeq=CLOBA011ZH06FP1&cluster=9703.f. Contact
cgi-bin/cluster.cgi?eeq=CLOBA011ZH06FP1&cluster=9703.f. Contact
Feng Liang Bmail: fliangolifetech.com URL:
http://fulllength.invitrogen.com/ InvitroGen Corporation 1600
Faraday Avenue Genoscope sequence ID: CLOBA011ZH06FP91.
Location/Qualifiers
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cgi-bin/cluster.cgi?seq=CL0BA009ZF09FPl&cluster=1095.f. Contact
Feng Liang Bmail: fliang@lifetech.com/NL:
http://fulllength.invitrogen.com/InvitroGen Corporation 1600
Faraday Avenu Genoscope sequence ID: CL0BA009ZF09FPI.
Location/Qualifiers
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more information about this cluster, see
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         17; Mismatches
                                                                                                                                                                                                      /organism="Homo sapiens"
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/mol_type="mRNA"
/db_xref="taxon:9606"
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Drosophila melanogaster genome survey sequence SP6 end of BAC BACNISHO of DrosBAC library from Drosophila melanogaster (fruit AL106008 AL106008 IG:5619558
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Submitted (13-JUJ-1999) Genoscope - Centre National de Sequencage :
BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
- Web : www.genoscope.cns.fr)
Determination of this BAC-end sequence was carried out as part of a collaboration with the European Drosophila Genome Project (EDGP) - http://www.edgp.ebi.ac.ut -. This Drosophila melanogaster BAC library (Dros BAC) was made by Alain Billaud at CBFH (Centre d'Etded ut Delymorphisme Humain) with funding provided by a MRC project grant. The DNA was prepared from embryos by Alain Bucheton and Genevieve Payan. It has been constructed in the vector
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           145 GAAAGCAACGCTTGAAAAAAGGAAAGTTAGCCCTATCGGGTATATTTTGGAAGTTGTAAA 204
                                                      206 TACTACRIGITCICTICIPAGICCCACTCCTCTTTTCTTTGAGCAGGAAAGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               146 AAAGCAACGCTTGAAAAAGGAAAGTTAGCCCTATCGGGTATATTTTGGAAGTTGTAAAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          26 ATTIATATGCTGATTTATGGGTGATTTTGCTTCCTTCTTTATACTTTTATTTCCCAA
                                                                                                                                                                                                                                                                                                                                                                                                                Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /organism="Drosophila melanogaster"
                                                                                                  205 ATACTACRIGITCTCTTCTAAGTCCCACTCCT 236
                                                                                                                        u
                                                                                                                                                                                                                                                                                                                                                                                            Drosophila melanogaster (fruit fly)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /mol_type="genomic DNA"
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/clone_lib="brosBaC"
/plasmid="pBeloBACI1"
/note="end : SP6"
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with a NotI-oligo(dT) primer. Five prime end enriched,
with a NotI-oligo(dT) primer. Five prime end enriched,
double-strand cDNA was digested with Not I and cloned into
the Not I and EcoNA wites of the pcMVSPORT 6 vector.
Library was not normalized.
177 APPARTA
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Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
1 (basea 1 to 1201)
Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
Pull-length cDNA libraries and normalization
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Email: segref@genoscope.cns.fr, Web: www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Library was constructed by Life Technologies, a division of
Library was constructed belongs to sequence cluster 7847.r For
more information about this cluster, see
http://www.genoscope.cns.fr/
cgi-bin/cluster.cgi?seq=CL0BB010ZG0IFP1&cluster=7847.r. Contact :
http://fulllength.invitrogen.com/ InvitroGen Corporation 1600
Faraday Avenue Genoscope sequence ID : CL0BB010ZG0IFP1.
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                                                                            27 TITATATGCTGATTTATGGGTGATTTTGCTTCCTTCTTTATACTTTTATTTCCCAAA
                                       Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Unpublished
On Feb 13, 2001 this sequence version replaced gi:12777915.
Contact: Genoscope Genoscope - Centre National de Sequencage
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46.2%; Pred. No. 3.3e+02;
iive 12; Mismatches 102; Indels
                                     51; Indels
                   6.8e+02;
                                     Mismatches
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/db_xref="taxon:9606"
/clone="CLOBB010ZG01"
             Pred. No.
                                                                                                                                                                                                                                                147 AAGCAACGCTTGAAAAAAGGAAA 169
                                                                                                                                                                                                                                                                          AAAAAAAAAAAAAAAAAA 103
49.0%; ELL
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EST.
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Matches 98; Conservative
                                70; Conservative
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/organism="Homo sapiens"
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/db_tref="mRNA"
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/db_tref="wexpon:9606"
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Library was not normalized."
Library was not normalized."
191 g 116 t 194 others
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Genoscope - Centre National de Sequencage
Benoscope - Centre National de Sequencage
BP 191 91006 EVRY Cedex - France
Bmail: seqretégenoscope.cns.fr, Web : www.genoscope.cns.fr
Email: seqretégenoscope.cns.fr, Web : www.genoscope.cns.fr
Invitzogen. This sequence belongs to sequence cluster 6437.r. For more information about this cluster, see
http://www.genoscope.cns.fr/
cgi-bh//cluster.cgi?seq=CLOBB012ZG0FP1&cluster=6437.r. Contact :
Feng Liang Email : filang@lifetech.com URL :
http://fulllength.invitrogen.com/ InVitroGen Corporation 1600
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BP 191 91006 EVRY cedex - France
BR 191 91006 EVRY cedex - France
BR 191 91006 EVRY cedex - France
BR 191 91006 EVRY cedex - France
Library was constructed by Life Technologies, a division of
Invitrogen. Contact : Feng Liang Email : fliang@lifetech.com URL :
http://fulllength.invitrogen.com/ InVitroGen Corporation 1600
Faraday Avenue Genoscope sequence ID : XCLOBB001ZA03FP1.

Location/Qualifiers
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 934)
Li, W.B., Gruber, C., Jessee, J., and Polayes, D.
Full-length cDNA libraries and normalization
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Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          9.9%; Score 52.2; DB 13; Length 1201;
31.5%; Pred. No. 3.5e+02;
tive 55; Mismatches 43; Indels 0;
                               1 (Dages 1 to 1201)
Li W.B., Gruber, C., Jessee, J. and Polayes, D.
Pull-length cDNA libraries and normalization
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                          (bases 1 to 1201)
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/db_xref="taxon:9606"
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/note="Vector: pCWV8PORT 6; lst strand cDNA was primed
with a NotI-oligo(dT) primer. Five prime end enriched,
double-strand cDNA was digested with Not I and cloned into
the Not I and EcoRV sites of the pCMVSPORT 6 vector.
Library was not normalized."
Library was not normalized. 234 others
                                                                                                                                                                              EST 13-MAY-2003
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Genoscope - Centre National de Sequencage
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: seqrefégenoscope.cns.fr, Web : www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. Contact: Feng Liang Email: fliang@lifetech.com URL:
Invitrogen. Contact: Feng Liang Email: fliang@lifetech.com URL:
Faraday Avenue Genoscope sequence ID : XCLOBA001ZE02FP1.
Location/Qualifiers
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 699)
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
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XCLOBB001ZA03 3-PRIME, mRNA sequence.
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BX424825 Homo sapiens PLACENTA Homo sapiens CDNA clone
XCLOBA001ZE02 3-PRIME, mRNA sequence.
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53.1%; Pred. No. 4.6e+02;
326 AAGGTGCAGCAGAGCCCTTTTCTTCCCAGG 355
                          854 WMCCACYCGBCCCCCYYYTAYTATCSGSS 825
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Homo sapiens
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the Not I and EcoRV sites of the pCMVSPORT 6 vector.
Library was not normalized."
140 c 113 g 196 t 105 others
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Xenopus laevis
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/mol_type="mRNA"
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/clone="IMAGE:6877304"
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                                                                                                        ch 9.8%;
1 Similarity 53.6%;
98; Conservative
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                                                                                                                                           /close type="NEUROBLASTOMA"
/close lib="Homo sapiens NEUROBLASTOWA"
/note="Vector: pcwySporr 6, 1st strand cDNA was primed
/note="Vector: pcwySporr 6, 1st strand cDNA was primed
with a NotI-oligo(dT) primer. Five prime end enriched,
double-strand cDNA was digested with Not I and cloned into
Library was not normalized." 188 others
1 184 c 192 g 142 t 188 others
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/clone_"Vector: pcMvSPORT & is strand cDNA was primed
with a NotI-oligo(dT) primer. Five prime end enriched,
double-strand cDNA was digested with Not I and cloned into
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.

    (bases 1 to 923)

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BP 191 91006 EVRY cedex - France
Emall: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 4504.f For
more information about this cluster, see
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    http://www.genoscope.cns.fr/
cgi-bin/cluster.cgi?seq=CL0BB012ZH03FP1&cluster=4504.f. Contact
cgi-bin/cluster.cgi?seq=CL0BB012ZH03FP1&cluster=4504.f. Contact
Feng Liang Email : fliangelifetech.com URL :
http://fulllength.invitrogen.com/ InvitroGen Corporation 1600
Faraday Avenue Genoscope sequence ID : CL0BB012ZH03FP1.
Location/Qualifiers
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BX425397 Homo sapiens NEUROBLASTOWA Homo sapiens CDNA clone CLOSB012ZH03 3-PRIME, mRNA sequence.
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Faraday Avenue Genoscope sequence ID : CLOBB012ZG07FP1.
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       132 AGAAAAAAAACTGAAAGCAACGCTTGAAAAAAGGAAA 169
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                                                                                  /mol_type="mRNA"
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Email: cgapba-r@mail.nih.gov

Email: cgapba-r@mail.nih.gov

Sequenced with vector primer

Tissue procurement: Drs. Donald Brown and Liquan Cai

Tissue procurement: Drs. Donald Brown and Liquan Cai

CDNA Library Preparation: CLOWTECH

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Agencourt Bioscience Corporation

Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:

http://image.llnl.gov

Plate: LLCM3115 row: 1 column: 07

High quality sequence stop: 158.

Location/Qualifiers

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/clone lib="NICHD XGC Tad1"
/clone lib="NICHD XGC Tad1"
/note="Organ: Developing Tadpole; Vector: pDNR-LIB;
Site 1: Sfi; Site 2: Sfi; S' and 3' adaptors were used in
cloning as follows: S' adaptor sequence:
S'-ATCTAGAGGCCAGGGGGGGCGCARG-GT(30) BN-3' (where B = A,
C, or G and N = A, C, G, or T). Average insert size 1.6 kb
(range 0,9-3.0 kb). 15/15 colonise contained inserts by
PCR. This library was enriched for full-length clones and
was constructed by Clontech Laboratories (Palo Alto, CA)."
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                                                                                                                                                                                                                                                                                                                     146 AAAGCAACGCTTGAAAAAAGGAAAGTTAGCCCTATCGGGTATATTTTGGAAGTTGTAAAA 205
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1 (Dases 1 to 964)

NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.

NATIONOC Gancer Institute, Cancer Genome Anatomy Project (CGAP), Unpublished
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        111 AAAAAAAAAAAAAAAAAAAAAAAAGGCGGCCGCTCTAGAGTWTCCCTCGAGGGCCCCAAGT 52
                                                                                                                                                                                                                                                                           0, Gaps
       DB 13; Length 923;
Score 51.8; DB 13; Length Pred. No. 4.5e+02; 4; Mismatches 81; Indels
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CNS030IZ 589 bp DNA linear GSS 01-SEP-2000 Tetraodon nigroviridis genome survey sequence T7 end of clone 043121 of library G from Tetraodon nigroviridis, genomic survey
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This sequence is a single read and was generated as part of a large scale clone-end sequencing project of the Tetraodon nigroviridis genome. For more information, please take a look at http://www.genoscope.cns.fr/Tetraodon.
                                                                                                                                                                                                                                                                                                                                                                                                                    Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi, Actinopterygii, Neopterygii, Teleostei, Buteleostei, Neoteleostei, Acanthomorpha, Acanthopterygii, Percomorpha, Tetraodontiformes, Tetradontoidea, Tetraodontidae, Tetraodon.
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Submitted (12-APR-2000) Genoscope - Centre National de Sequencage :
BP 191 91006 EVRY cedex - FRANCE (E-mail : segref@genoscope.chs.fr
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                      62 CITIAIACTITIAITCTAAATTITICTTAAGCAAATTITICTTAGCIAATCAATA 121
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Roest Crollius, H., Jaillon, O., Dasilva, C., Ozouf-Costaz, C., Fizames, C., Fischer, C., Bouneau, L., Billault, A., Quetier, F., Sautin, W., Bernot, A. and Weissenbach, O. Characterization and repeat analysis of the compact genome of the freshwater pufferfish Tetracdon nigroviridis
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Roest Crollius, H., Jaillon, O., Dasilva, C., Bouneau, L., Fisher, C Bernot, A., Fizames, C., Wincker, P., Brottier, P., Quetier, F., Saurin, W. and Weissenbach, J.
Estimate of human gene number provided by genome-wide analysis using Tetraodon nigroviridis DNA sequence
NAT. Genet. 25 (2), 235-238 (2000)
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Length 589;
                                                                                                           Indels
                                                                  123 ATTATCAAAAGAAAAAAAAACTGAAAGCAACGCTTGAAAAAAGGAAA
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/organism="Tetraodon nigroviridis"
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GSS; genome survey sequence.
Tetraodon nigroviridis
Tetraodon nigroviridis
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /tissue type="PLACENTA"
/clone lib="Homo sapiens PLACENTA"
/clone lib="Homo sapiens PLACENTA"
/note="Vector: pCMVSPORT 6; lst strand cDNA was primed
with a Not1-oligo(dT) primer. Five prime end enriched,
double-strand cDNA was digested with Not I and cloned into
the Not I and EcoRV sites of the pCMVSPORT 6 vector.
Library was not normalized."
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65 others
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BX424931 Homo sapiens PLACENTA Homo sapiens CDNA clone CL0BA004ZC11
3-PRIME, mRNA sequence.
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                                                                                                                                                                                                                                                                                        63 ITTATACTTTTATTCCCAAATTTTTCTTAAGCAAATATTTCTTTGCTAATCAATAA 122
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 512)
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BP 191 91006 EVRY cedex - France
BR 191 91006 EVRY cedex - France
BR 191 91006 EVRY cedex - France
BR 191 91006 EVRY cedex - France
Brail: seqref@genoscope.cns.fr, web: www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 1009.f For
more information about this cluster, see
http://www.genoscope.cns.fr/
cgi-bin/cluster.cgi?seq=CL0BA004ZC11FP1&cluster=1009.f. Contact :
Feng Liang Email: fliang@lifetech.com URL :
http://fullength.invitrogen.com/ InvitroGen Corporation 1600
Faraday Avenue Genoscope sequence ID : CL0BA004ZC11FP1.
                                                                                                                                                                                                  31 ԷՐդեձերը դրդորդորդորդորդորդորդորդուհիրարիարարդորդորդորդորդորդորդ
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                                                                                                               Gaps
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                                                                                                                                                                                                                                                                                                                                    132 AGAAAAAAAACTGAAAGCAACGCTTGAAAAAAAGGAAAGTTAGCCCTATC 181
                                                                    964;
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49.1%; Pred. No. 6.9e+02;
                                                                    Length
                                                                                                             Indels
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                                                                      14;
                                                                    Score 51.6; DB 14
Pred. No. 4.7e+02;
                                                                                                               0; Mismatches
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    129
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/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CLOBA004ZC11"
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      224
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                                                                    9.8%;
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                                                                                                             96; Conservative
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/db xref="taxon:9606"
/clone="CLOBAG062C11"
/tissue type="FLACENTA"
/clone_lib="Homo sapiens PLACENTA"
/clone_lib="Homo sapiens PLACENTA"
/note="Vector: pCMVSPORT 6; lst strand cDNA was primed
with a Not1-oligo(dT) primer. Five prime end enriched,
double-strand cDNA was digested with Not I and cloned into
Library was not normalized."
                                                                                                                                                                              AL513907 738 bp mRNA linear EST 08-MAY-2003
AL513997 Homo sapiens PLACENTA Homo sapiens cDNA clone CLOBA006ZCll
3-PRIME, mRNA sequence.
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                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1. (bases 1 to 738)
1.4, W.B., Gruber, C., Jessee, J. and Polayes, D.
Full-length cDNA libraries and normalization
Ombublished
On Feb 13, 2001 this sequence version replaced gi:12777401.
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BP 191 91006 EVRY cedex - France
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 9836.r For
more information about this cluster, see
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       http://www.genoscope.cns.fr/
cgi-bin/cluster.cgi?eeq=CLOBA006ZC11FP1&cluster=9836.r. Contact
Feng Liang Email : filang@lifetech.com URL :
http://fulllength.invitrogen.com/ InVitroGen Corporation 1600
Faraday Avenue Genoscope sequence ID : CLOBA006ZC11FP1.
Location/Qualifiers
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52.0%; Pred. No. 6.1e+02;
.ive 14; Mismatches 57; Indels
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                                                                                 182 GGGTATATTT 192
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RESULT 26

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PRESENCE MY CERONOLITE HOrdoum vulgare seedling green leaf EST library
MCDDAROON (Blameria challenged) Hordoum vulgare subbp. vulgare
MCCESSON
WAS CHONE HY_CEROLOLITE, MRNA sequence.

BEGGHAI. GI.11195935
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plasmid vector. The DH10B E. Coli host was trassiformed with ligation mixture by the standard chemical method. The worsage insert size is about 1.9 kb. The library was constructed by talan Piao (NIA)."

164 C 204 g 242 t 71 others
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                                                                                                                                                                                                                                                                                                                                       77 TATTCCCAAATTTTTCTTAAGCAAATATTTCTTTGCTAATCAATAAATTATCAAAAGAAA 136
                                                                                                                                                                                                                                                                                                                                                                                 137 AAAAAACTGAAAGCAACGCTTGAAAAAAGGAAAGTTAGCCCTATCGGGTATATTTTGGAA 196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /clone="CSODJOGYL14"
/cell type="T CELLS (JURKAT CELL LINE) COT 10-NORWALIZED"
/cell_line="JURKAT"
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1 113 c 140 g 173 t
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 927)
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Genoscope - Centre National de Sequencage
Bp 191 91006 EVRY cedex - France
Email: seqrefégenoscope.cns.fr, Web : www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 155.r For
more information about this cluster, see
http://www.genoscope.cns.fr/
cgi-bin/cluster.cgi?seq=CSOBAHO16ZE09FM1&cluster=355.r. Contact :
Feng Liang Email : fliang@lifetech.com URL :
http://fulllength.invitrogen.com/ InvitroGen Corporation 1600
Faraday Avenue Genoscope sequence ID : CSOBAHO16ZE09FM1.
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10-NORMALIZED"
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                                                                                                                                                                                                                                                                                           th 9.7%; Score 51.2; DB 12; Length 856; Similarity 42.2%; Pred. No. 5.6e+02; 92; Conservative 0; Mismatches 126; Indels 0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               196 GCGGAGAAAAATAATTTTTTTTTTTCCCCCCCCC 233
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        197 GITGTAAAATACTACRIGITCTCTTCTAAGTCCCACTC
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Matches 92; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     BM115165 856 bp mRNA linear EST 30-JAN-2002 LOGISED8-3 NIA Mouse Newborn Brain cDNA Library Mus musculus cDNA clone L0816E08 3', mRNA sequence.
BM115165
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                                                                                                                                                                                                                   160 AAAAAGGAAAGTTAGCCCTATCGGGTATATTTTGGAAGTTGTAAAATACTACRTGTTCTC 219
                                                                                                                                                                                                                                                                                                                  Mus musculus (house mouse)
Mus musculus
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mummalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 856)
Piao, Y., Kargul, G.J., Dudekula, D.B., Qian, Y., Pantano, S., Lim, M.K.
and Ko, M.S.H.
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                                                                                            Gaps
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National Institute on Aging/National Institutes of Health
333 Cassell Drive, Suite 4000, Baltimore, MD 21224-6820, USA
Email: cdna@lgsun.grc.nia.nih.gov
Plate: L0816 row: E column: 08
Seg primer: -21M13 Forward
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    Length 838;
                                                Indels
  Score 51.2; DB 10;
Pred. No. 5.7e+02;
1; Mismatches 86;
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/strain="CS7BL/G"
/db_xref="niaEST:L0816E08-3"
/db_xref="taxon:10090"
/clone="L0816E08"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /tissue_type="Newborn Brain"
/dev_stage="Newborn"
/lab_host="DH10B"
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/organism="Mus musculus"
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High quality sequence stop: 856
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  Query Match 9.7%;
Best Local Similarity 53.7%;
Matches 101; Conservative
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/tissue type="NEUROBLASTOWA"
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/clone lib="Homo sapiens NEUROBLASTOWA"
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/double-strand cDNA was digested with Not I and cloned into
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381 bp mRNA linear EST 15-MAY-2003
BX425197 Homo sapiens NEUROBLASTOMA Homo sapiens cDNA clone
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
1 (bases 1 to 381)
Li, W.B., Gruber, C., Jessee, J. and Polayes, D.
Full-length cDNA libraries and normalization
Unpublished
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BP 191 91006 EVRY cedex - France
Bmail: seqref@genoscope.cns.fr, web : www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 6437.r For
more information about this cluster, see
http://www.genoscope.cns.fr/
cgi-bin/cluster.cgi?seq=CLOBB003ZH07FPl&cluster=6437.r. Contact :
Feng Liang Email : flang@lifetech.com URL :
http://fulllength.invitrogen.com/ InvitroGen Corporation 1600
Faraday Avenue Genoscope sequence ID : CLOBB003ZH07FPl.
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/clone Lib="Homo sapiens PLACENTA"
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with a NotI-oligo(dT) primer. Five prime end enriched,
double-strand cDNA was digested with Not I and cloned into
the Not I and EcoRV sites of the pCMVSPORT 6 vector.
Library was not normalized."
12 cothers
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Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
BP 191 91006 EVRY cedex - France
Email: segrefagenoscope.cns.fr, Web: www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 9703.f For
more information about this cluster, see
http://www.genoscope.cns.fr/
cgi-bin/cluster.cgi?seq=CL0BA011ZH06FP1&cluster=9703.f. Contact:
Feng Liang Email: fliang@lifetech.com URL:
http://fulllength.invitrogen.com/ InvitroGen Corporation 1600
Faraday Avenue Genoscope sequence ID: CL0BA011ZH06FP1.
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234 bp mRNA linear EST 15-MAY-2003
BX425129 Homo sapiens PLACENTA Homo sapiens cDNA clone CLOBA011ZH06
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                                                                                                                                                                                                                   196 АААЛАЛАЛАЛАЛАЛАЛАЛАЛАЛАЛАССССТАТ
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9.6%; Score 50.8; DB 13; Length 927;
53.5%; Pred. No. 6.1e+02;
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BX425129.1 GI:30780435
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Matches 106; Conservative
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Library was not normalized."

158 c 203 g 237 t 62 others
AL543011 Homo sapiens PLACENTA Homo sapiens cDNA clone CSODE013YL225-PRIME, mRNA sequence.
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1. (bases 1 to 894)
1.i., W.B., Gruber, C., Jessee, J. and Polayes, D.
Full.length cDNA libraries and normalization
                                                                                                                                                                                                                                         On Feb 15, 2001 this sequence version replaced gi:12875489. Contact: Genoscope Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of Invitrogen. This sequence belongs to sequence cluster 9876.f For more information about this cluster, see http://www.genoscope.cns.fr/
cgi-bin/cluster.cgi?seq=CS00EGI3DF11QP1&cluster=9876.f. Contact:
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http://fulllength.invltrogen.com/ invltroGen Corporation 1600
Faraday Avenue Genoscope sequence ID: CSODE013DF11QP1.
Location/Qualifiers
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11.5%; Pred. No. 6.7e+02;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /organism="Homo sapiens"
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                                                        AL543011.2 GI:30548727
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                                                                                             Homo sapiens (human)
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with a NotI-oligo(dT) primer. Five prime end enriched,
double-strand CDNA was digested with Not I and cloned into
the Not I and EcoRV sites of the pCMVSPORT 6 vector.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 332)
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                                                                                                                                                                                                                    Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 6609.f For
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BP 191 91006 EVRY cedex - France
Email: sequeféquencope.cns.fr, Web : www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 6437.r For
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cgi.bin/cluster.cgi?seq=CLOBA009ZCO8FPl&cluster=6609.f. Contact
cgi.bin/cluster.cgi?seq=CLOBA009ZCO8FPl&cluster=6609.f. Contact
Feng Liang Email : fliang@lifetech.com URL :
http://fulllength.invitrogen.com/ InvitroGen Corporation 1600
Faraday Avenue Genoscope sequence ID : CLOBA009ZCO8FP1.
Location/Qualifiers
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Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
Full-length cDNA libraries and normalization
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Contact: Genoscope
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Interpret the control of the sequence version replaced gi:12777469.

On Feb 13, 2001 this sequence version replaced gi:12777469.

Contact: Genoscope Genoscope Genoscope - Centre National de Sequencage Genoscope - Centre National de Sequencage BP 191 91006 EVRY cedex - France Email: seqrégéenoscope.cns.fr, Web: www.genoscope.cns.fr Library was constructed by Life Technologies, a division of Invitrogen. This sequence belongs to sequence cluster 7629.r For more information about this cluster, see http://www.genoscope.cns.fr/ cgi-bin/cluster.cgi?seq=CLOBA011ZE10FP1Kcluster=7629.r. Contact : Feng Liang Email: fliang@lifetech.com URL: Feng Liang Email: fliang@lifetech.com URL: http://fulllength.invitrogen.com/ InvitroGen Corporation 1600 Faraday Avenue Genoscope sequence ID: CLOBA011ZE10FP1.
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/note="Vector: pcMVSPORT_6; lst strand cDNA was riched,
double-strand cDNA was digested with Not I and cloned double-strand cDNA was digested with Not I and cloned into
Library was not normalized."
115 c 106 g 188 t 138 others
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AL513975 Homo sapiens PLACENTA Homo sapiens cDNA clone CL0BA011ZE10
3-PRIME, mRNA sequence.
AL513975.2 GI:30463860
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double-strand cDNA was digested with Not I and cloned into
the Not I and EcoRV sites of the pCMVSPORT 6 vector.
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Li W. B., Gruber, C., Jessee, J. and Polayes, D.
Full-length cDNA libraries and normalization
                                                                                                                                                                                                                                                                                                                                                        27 TITATATGCTGATTTATGGGTGATTTTGCTTCCTTCTTTATACTTTTATTTCCCAAA
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                                                                                                                                                                                                                                                          13;
                                                                                                                                                                                                                                                        Score 50.4; DB 13.
Pred. No. 6.9e+02;
3; Mismatches 54
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/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            147 AAGCAACGCTTGAAAAA 164
                                                                                                                                                                                                                                                     ch 9.5%;
1 Similarity 58.7%;
81; Conservative
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/mol Lype="mixmo" supremark
/clone="CLOBB003ZH07"
/tissue type="mixmo sapiens NEUROBLASTOMA"
/clone lib="Homo sapiens NEUROBLASTOMA"
/clone lib="Homo sapiens NEUROBLASTOMA"
/clone lib="Homo sapiens NEUROBLASTOMA"
/with a NorI-oligo(dT) primer. Five prime end enriched,
double-strand cDNA was digested with Nor I and cloned into
the Nor I and EcoRV sites of the pCMVSPORT 6 vector.
Liberty was not normalized." 89 others
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Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: seqrefégenoscope.cns.fr, Web : www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 1357.r For
more information about this cluster, see
                       http://www.genoecope.cns.fr/
cgi-bin/cluster.cgi?seq=CLOBB003ZH07FPl&cluster=6437.r. Contact
cgi-bin/cluster.cgi?seq=CLOBB003ZH07FPl&cluster=6437.r. Contact
Feng Liang Email : fliang@lifetech.com/UR. :
http://fulllength.invitrogen.com/ InvitroGen Corporation 1600
Faraday Avenue Genoecope sequence ID : CLOBB003ZH07FP1.
Location/Qualifiers
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cgi-bin/cluster.cgi?aeq=CLi0BB027ZB08FPl&cluster=1357.r. Contact
Feng Liang Email : filang@lifetech.com URL :
http://fulllength.invitrogen.com/ InvitroGen Corporation 1600
Faraday Avenue Genoscope sequence ID : CL0BB027ZB08FPl.
Location/Qualifiers
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     more information about this cluster, see
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/mol_type="mRNA"
/db_xrefe"taxon:9606"
/clone="CLOBB027ZB08"
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661 bp mRNA linear EST 08-MAY-2003 Homo mapiens PLACENTA Homo mapiens cDNA clone CLOBA011ZG02
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(Dases 1 to 661)

Li,W.B., Gruber,C., Jessee,J. and Polayes,D.

Ext. Length cDNA libraries and normalization
Unpublished

On Feb 13, 2001 this sequence version replaced gi:12777509.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: seqrefégenoscope.cns.fr, Web : www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 108.r For
more information about this cluster, see
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              http://www.genoscope.cns.fr/
cgi-bin/cluster.cgi?eeq=CLOBA011ZG02FP1&cluster=108.r. Contact
cgi-bin/cluster.cgi?eeq=CLOBA011ZG02FP1&cluster=108.r. Contact
Feng Liang Email : fliang@lifetech.com URL :
http://fulllength.invitrogen.com/ InVitroGen Corporation 1600
Faraday Avenue Genoscope sequence ID : CLOBA011ZG02FP1.
Location/Qualifiers
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                                           206 AAAAAAAAAAAAAAAAAAAAAA 184
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BX349610.1 GI:30365363
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AL514015
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Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
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BP 191 91006 EVRY cedex - France
BP 191 91006 EVRY cedex - France
BP 191 91006 EVRY cedex - France
BP 191 91006 EVRY cedex - France
Email: sequence belongs to sequence cluster 7985.fr
Invitrogen. This sequence belongs to sequence cluster 7985.fr For
more information about this cluster, see
http://www.genoscope.cns.fr/
cgi-bin/cluster.cgi'sseq=CiubBB015ZCI0FP1kcluster=7985.f. Contact :
Fong Liang Email: fliang@lifetech.com URL :
Fong Liang Email: fliang@lifetech.com URL :
http://fulllength.invitrogen.com/ Invitroden Corporation 1600
Faraday Avenue Genoscope sequence ID : CLOBB015ZCI0FP1.
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/clone_lib="Homo sapiens NEUROBLASTOMA"
/clone_Type="Homo sapiens NEUROBLASTOMA"
/note="Vector: pcWVSPORT 6; lst strand cDNA was primed with a Not1-oligo(dI) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoRV sites of the pcMVSPORT 6 vector.
Library was not normalized."
20 c 172 t 20 others
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Li, W.B., Gruber, C., Jessee, J. and Polayes, D. Full-length cDNA libraries and normalization Unpublished
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Pred. No. 6.1e+02;
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8; Mismatches 56
                                           72; Conservative 19; Mismatches
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/db_xref="taxon:9606"
/clone="CL0BB015ZC10"
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                    49.38;
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/organism="Homo sapiens"
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Best Local Similarity 55.2
Matches 79; Conservative
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3-PRIME, mRNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /tissue type="PiACENTA COT 25-NORMALIZED"
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primer. Five prime end enriched, double-strand cDNA was
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sites of the pCWVSPORT 6 vector. Library was normalized.
79 c 53 g 378 t 30chers
                                                    Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                   Email: seqref@genoscope.cns.fr. Web : www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 7295.f For
more information about this cluster, see
http://www.genoscope.cns.fr/
cgi-bin/cluster.cgi?seq=CSOBAH013ZG04FM1&cluster=7295.f. Contact
feep Liang Email : fliang@lifetech.com URL :
http://fulllength.invitrogen.com/ InvitroGen Corporation 1600
Faraday Avenue Genoscope sequence ID : CSOBAH013ZG04FM1.
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Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
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                                                                                        1 (bases 1 to 1024)
Li.W.B., Gruber, C., Jessee, J. and Polayes, D.
Full-length cDNA libraries and normalization
                                                                                                                                                                Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
                                                                                                                                                                                                                                                                                                                                                                                                                                 /organism="Homo sapiens"
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/clone Inb="Homo sapiens PLACERTA"
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/note="Vector: pCMVSPORT 6; lst strand cDNA was primed
/note="Vector: pCMVSPORT 6; lst strand cDNA was digested with Not I and cloned into
the Not I and EcoRV sites of the pCMVSPORT 6 vector.
Library was not normalized."
143 c 36 g 250 t 208 others
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AL513719 Homo sapiens PLACENTA Homo sapiens cDNA clone CL0BA007ZH01
3-PRIME, mRNA sequence.
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gq-bin/cluster.cg1?seq=CDBA004ZG10FP1&cluster=2672.f. Contact :
gq-bin/cluster.cg1?seq=CDBA004ZG10FP1&cluster=2672.f. Contact :
Feng Liang Email : fliangelifetech.com URL :
http://fulllength.invitrogen.com/ InvitroGen Corporation 1600
Faraday Avanue Genoscope sequence ID : CLOBA004ZG10FP1.
Location/Qualifiers
1. .1126
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Li, W.B., Gruber, C., Jessee, J., and Polayes, D.
Full-length cDNA libraries and normalization
Unpublished
On Feb 13, 2001 this sequence version replaced gi:12777213.
Contact: Genoscope
Genoscope - Centre National de Sequencage
Genoscope - Prance
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Library was constructed by Life Technologies, a division of Invitrogen. This sequence belongs to sequence cluster 2672.f For more information about this cluster, see
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Library was constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 817.f For
more information about this cluster, see
http://www.genoscope.cns.fr/
cgi-bin/cluster.cgi?seq=CirOBA007ZH01FP1&cluster=817.f. Contact ::
Feng Liang Email : fliang@lifetech.com URL :
http://fulllength.invitrogen.com/ InvitroGen Corporation 1600
Faraday Avenue Genoscope sequence ID : CLOBA007ZH01FP1.
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Pred. No. 6.7e+02;
8; Mismatches 56
                                                                                                                                                                                                                                                                                                                                   /organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                                                              /mol_type="mRNA"
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Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 ENTX redex - France
Email: sequencepe.cns.fr, whe : www.genoscope.cns.fr
was not normalized. Library was constructed by Life Technologies, a
division of Invitrogen. This sequence belongs to sequence cluster
1731.f For more information about this cluster, see
http://www.genoscope.cns.fr
cgi-bin/cluster.cgi?seq=XCLOBB001ZE02FP1&cluster=1731.f. Contact:
Feng Liang Email: filiangelifetech.com URL:
http://tullnength.invitrogen.com/ InvitroGen Corporation 1600
Faraday Avenue Genoscope sequence ID: XCLOBB001ZE02FP1.
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/clone lib="Homo sapiens NEUROBLASTOWA"
/clone lib="Homo sapiens NEUROBLASTOWA"
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/with a NotI-oligo(dT) primer. Five prime end enriched,
double-strand cDNA was digested with Not I and cloned into
the Not I and ECORV sites of the pCMVSPORT 6 vector.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 1201)
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53.1%; Pred. No. 6.5e+02;
ive 12; Mismatchės 55; Indels 0;
                                                           Length 1189;
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                                                        Score 50.2; DB 9;
Pred. No. 6.5e+02;
9; Mismatches 72;
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                                                           9.5%;
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On Feb 13, 2
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with a NotI-oligo(dT) primer. Five prime end enriched,
double-strand cDNA was digested with Not I and cloned into
Library was not normalized."
226 c 199 g 222 t 208 others
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BF 191 91006 EVRY cedex - France
BF 201 91006 EVRY cedex - France
BF 201 91006 EVRY cedex - France
BF 201 91006 EVRY cedex - France
BF 201 91006 EVRY cedex - France
Library was constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 1883.f For more information about this cluster, see
Mttp://www.genoscope.cns.fr/
cgi-bin/cluster.cgi?seq=CLOBA009ZB08FPL&cluster=1883.f. Contact :
Feng Liang-Ernal : filang@lifetech.com URL :
http://fulllength.invitrogen.com/ InVitroGen Corporation 1600
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Location/Qualifiers
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1 (bases 1 to 1189)
Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
Prill-length CDNA libraries and normalization
Unpublished
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/closue type="PLACENTA"
/close lib="Homo sapiens PLACENTA"
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with a NotI-oligo(dT) primer. Five prime end enriched,
double-strand cDNA was digested with Not I and cloned into
the Not I and EcoxV sites of the pCMVSPORT 6 vector.
Library was not normalized."
18 c 19 g 130 t 27 others
                                                                           294 bp mRNA linear EST 22-MAY-2003
BX46415 Homo sapiens PLACENTA Homo sapiens cDNA clone CLOBA005ZH05
3-PRIME, mRNA sequence.
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BP 191 91006 EVRY cedex - Prance
Library was constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 5229.r For
http://www.genoscope.ns.fr/
cg1-bin/cluster.cg1?seq=CLOBA005ZH05FP1&cluster=5229.r. Contact ::
Feng Liang Email : fliangelifetech.com URL :
http://tulllength.invitrogen.com/ InVitroGen Corporation 1600
Faraday Avenue Genoscope sequence ID : CLOBA005ZH05FP1.
                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 294)
1 'Liw.Bu, Gruber,C., Jessee,J. and Polayes,D.
Full-length cDNA libraries and normalization
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Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage :
BP 191 91006 EWYR cedex - FRANCE (B-mail : seqref@genoscope.cns.fr - Web : www.genoscope.cns.fr)
- Web : www.genoscope.cns.fr)
Determination of this BAC-end sequence was carried out as part of a collaboration with the Berkeley Drosophila Genome Project (BDGP).

The BDGP is constructing a physical map of the Drosophila melanogaster genome using these BACs. For further information please see http://www.fruitfly.org The BDGP Drosophila melanogaster BAC library was prepared by Kazutoryo Goeegawa and Aaron Mammoser in Pieter de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, NY. The library is named RPCI-98 and was constructed by partial EcoRI digestion of Drosophila DNA provided by the BDGP from the isogenic strain y2; cn bw sp, the same strain used for the BDGP's and how to order individual BAC clones, the entire library, or filters for hybridization from the BACPAC Resource Center can be found at http://bacpac.med.buffalo.edu/drosophila_bac.htm.
                                                                                                                                                                                                                                  928 bp DNA linear GSS 04-JUN-1999 Brosophila melanogaster genome survey sequence T7 end of BAC # BACK27244 of RPCI-98 library from Drosophila melanogaster (fruit AL071865
TITIGCTICCTICTITATACTITIATITACCAAATTITICCTAAGCAAATATTICTT 109
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Eukaryota, Metazoa, Arthropoda, Hexapoda, Insecta, Pterygota,
Neoptera, Endopterygota, Diptera, Brachycera, Muscomorpha,
Ephydroidea, Drosophilidae, Drosophila.
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9.5%; Score 50; DB 29; Length 928;
Best Local Similarity 31.3%; Pred. No. 7.9e+02;
Matches 62; Conservative 59; Mismatches 77; Indels
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/mol_type="genomic DNA"
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/note="end : T7"
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Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: seqrefégenoscope.cns.fr, Web: www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Library was constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 1769.f For
more information about this cluster, see
http://www.genoscope.cns.fr/
cgi-bin/cluster.cgi?seqaxCLOBA0012B11FP1&cluster=1769.f. Contact :
Feng Liang Email : fliang@lifetech.com URL :
Feng Liang Email : fliang@lifetech.com URL :
http://fulllength.invitrogen.com/ InvitroGen Corporation 1600
Faraday Avenue Genoscope sequence ID : XCLOBA001ZB11FP1.
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Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
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Li W. Gruber, C., Jessee, J. and Polayes, D.
Full-length cDNA libraries and normalization
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Sequence 8192, Ap

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Sequence 1033, Ap Sequence 12673, A Sequence 12673, A Sequence 11622, A Sequence 9335, Ap Sequence 11622, A Sequence 11099, A Sequence 110999, A Sequence 10999, A Sequence 5099

Sequence 141, App Sequence 1580, Ap Sequence 257, App Sequence 4844, Ap Sequence 11141, Ap

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Sequence 8414, Ap Sequence 11146, Ap Sequence 11782, A Sequence 17782, A Sequence 17782, A Sequence 1788, A Sequence 1788, A Sequence 66, Appl Sequence 66, Appl Sequence 1788, A Sequence 1789, Ap Sequence 1789, Ap Sequence 1789, Ap Sequence 1789, Ap Sequence 1789, Ap Sequence 1789, Ap Sequence 1789, Ap Sequence 1789, Ap Sequence 1789, Ap Sequence 1785, Appl Sequence 1785, Appl Sequence 1785, Appl Sequence 1786, Appl Sequence 1786, Appl Sequence 1786, Appl Sequence 1786, Appl Sequence 1786, Appl Sequence 1786, Appl Sequence 1786, Appl Sequence 1786, Appl Sequence 1786, Appl Sequence 1789, Ap Sequence 1789, Ap Sequence 1789, Ap Sequence 1789, Ap Sequence 1789, Ap Sequence 18904, Ap Sequence 1891, Ap Sequence 18914, Ap Sequence

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Matches 529; Conservative
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ORGANISM: Human
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Sequence 33, Appl
Sequence 33, Appl
Sequence 33, Appl
Sequence 33, Appl
Sequence 34, Appl
Sequence 4, Appl
Sequence 1004, Ap
Sequence 18604, Ap
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GENERAL INFORMATION:

APPLICANT: Wang, David G.

TITLE OF INVENTION: Identification and Mapping of Single Nucleotide

TITLE OF INVENTION: Polymorphisms in the Human Genome

FILE REFERENCE: 108827.129

CURRENT APPLICATION NUMBER: US/01027,632

CURRENT FILING DATE: 2002-04-30

PRIOR PELLING DATE: 2000-07-129

PRIOR PELLING DATE: 2000-07-129

PRIOR APPLICATION NUMBER: US 60/199,676

PRIOR APPLICATION NUMBER: US 60/199,483

PRIOR PELLING DATE: 2000-02-24

PRIOR PELLING DATE: 2000-02-24

PRIOR FILING DATE: 1999-11-23

PRIOR PELLING DATE: 1999-11-23

PRIOR PELLING DATE: 1999-09-18

PRIOR PELLING DATE: 1999-09-18

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                  US-09-814-353-17553
US-09-825-224-33
US-09-970-966-33
US-10-361-811-33
US-10-361-811-33
US-10-71-813-33
US-09-754-877-33
US-09-754-877-33
US-09-960-352-1004
US-09-914-353-17818
US-09-814-353-18604
US-09-814-353-18604
                                                                                                                                                                                                                                                                                                                                                   ALIGNMENTS
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Best Local Similarity 100.
Matches 529; Conservative
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ORGANISM: Human
RESULT 1
US-10-027-632-1
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US-10-027-632-300106

Sequence 300106, Application US/10027632

Publication No. US20030204075A9

GENERAL INFORMATION:
APPLICANT: Wang, David G.
TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
FILE REFERENCE: 108827.129

CURRENT APPLICATION NUMBER: US 60/128,006

PRIOR FILING DATE: 2000-07-12

PRIOR FILING DATE: 2000-07-12

PRIOR FILING DATE: 2000-04-20

PRIOR FILING DATE: 2000-04-20

PRIOR PLICATION NUMBER: US 60/185,218

PRIOR PLICATION NUMBER: US 60/185,218

PRIOR FILING DATE: 1099-09-28

PRIOR FILING DATE: 1999-09-28

PRIOR FILING DATE: 1999-09-28

PRIOR PLICATION NUMBER: US 60/146,002

PRIOR FILING DATE: 1999-09-28

PRIOR PLICATION NUMBER: US 60/146,002

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100.0%; Pred. No. 2.6e-119;
tive 0; Mismatches 0;
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Best Local Similarity 100.
Matches 528; Conservative
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; ORGANISM: Human
US-10-027-632-300106
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Sequence 54345, Application US/10027632

Sequence 54345, Application US/10027632

Sequence 54345, Application US/20030204075A9

GENERAL INFORMATION:
TITLE OF INVENTION: Identification and Mapping of Single Nuclectide
TITLE OF INVENTION: Identification and Mapping of Single Nuclectide
TITLE OF INVENTION: Identification and Mapping of Single Nuclectide
TITLE OF INVENTION: Identification and Mapping of Single Nuclectide
FILE REFERENCE: 108827.129

CURRENT PILING DATE: 2002-04-30

PRIOR APPLICATION NUMBER: US 60/198,676

PRIOR PILING DATE: 2000-07-12

PRIOR PILING DATE: 2000-03-29

PRIOR PILING DATE: 2000-03-29

PRIOR PELING DATE: 2000-03-29

PRIOR PELING DATE: 2000-03-29

PRIOR PELING DATE: 2000-03-29

PRIOR PILING DATE: 1999-11-33

PRIOR PILING DATE: 1999-11-33

PRIOR PILING DATE: 1999-11-33

PRIOR PILING DATE: 1999-11-33

PRIOR PILING DATE: 1999-11-33

PRIOR PILING DATE: 1999-10-80

PRIOR PILING DATE: 1999-11-33

PRIOR PILING DATE: 1999-11-33

PRIOR PILING DATE: 1999-11-33

PRIOR PILING DATE: 1999-18-30

SOFTWARE: FestSEQ for Windows Version 4.0

SEQ ID NO 54345
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Best Local Similarity 100.
Matches 528; Conservative
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US-10-027-632-54345
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APPLICANT: Wang, David G.
TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
ITILE OF INVENTION: Polymorphisms in the Human Genome
ITILE OF INVENTION: Polymorphisms in the Human Genome
FILE REFERENCE: 108827.129
CURRENT APPLICATION NUMBER: US/10/027,632
CURRENT PLING DATE: 2002-04-30
PRIOR PRIOR PELING DATE: 2000-07-29
PRIOR PRIOR DATE: 2000-04-20
PRIOR PRIOR DATE: 2000-04-20
PRIOR PRIOR DATE: 2000-03-24
PRIOR PLING DATE: 1999-11-23
PRIOR PLING DATE: 1999-11-23
PRIOR PLING DATE: 1999-11-23
PRIOR PLING DATE: 1999-10-24
PRIOR PLING DATE: 1999-08-09
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PRIOR APPLICATION NUMBER: US 60/146,002
PRIOR APPLICATION NUMBER: US 60/146,002
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PRIOR APPLICATION NUMBER: US 60/146,002
PRIOR PLING DATE: 1999-08-09
PRIOR PLING DATE: 1999-08-09
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100.0%; Pred. No. 2.6e-119;
ive 0; Mismatches 0;
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; GENERAL INFORMATION:
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Best Local Similarity
Matches 528; Conserv
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US-10-027-632-300106
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GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
TITLE OF INVENTION: Polymorphisms in the Human Genome
TITLE OF INVENTION: Polymorphisms in the Human Genome
TITLE OF INVENTION: Polymorphisms in the Human Genome
FILE REPREBRICE: 108827.129
CURRENT APPLICATION NUMBER: US/10/027,632
CURRENT APPLICATION NUMBER: US 60/218,066
FRIOR FILING DATE: 2000-04-20
FRIOR FILING DATE: 2000-04-20
FRIOR PEDLICATION NUMBER: US 60/193,483
FRIOR FILING DATE: 2000-03-29
FRIOR FILING DATE: 2000-03-29
FRIOR FILING DATE: 1999-11-23
FRIOR FILING DATE: 1999-01-23
FRIOR FILING DATE: 1999-08-09
FRIOR FILING DATE: 1999-08-09
SUPUMBER OF SEQ ID NOS: 325720
SUPUMBER OF SEG ID NOS: 325720
SUPUMBER OF SEG FOR WINDGMS VERSION 4.0
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Gaps
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100.0%; Pred. No. 2.6e-119;
iive 0; Mismatches 0;
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Matches 528; Conservative
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Best Local Similarity
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; ORGANISM: Human
US-10-027-632-54345
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US-10-027-632-54345
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 17876, Application US/09814353
Fublication No. US20030165831A1
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Leo, John
APPLICANT: Thompson, Pamela
APPLICANT: Lillie, James
TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS FOR
TITLE OF INVENTION: THERAPY OF OVARIAN CANCER
FILE REFERENCE: MRI-006B
CURRENT APPLICATION NUMBER: US/09/814,353
CURRENT FILING DATE: 2001-03-21
PRIOR FILING DATE: 2000-03-21
PRIOR FILING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: US 60/191,031
PRIOR FILING DATE: 2000-05-25
PRIOR APPLICATION NUMBER: US 60/211,940
PRIOR FILING DATE: 2000-06-15
PRIOR FILING DATE: 2000-07-07
PRIOR FILING DATE: 2000-07-07
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    147 AAGCAACGCTTGAAAAAGGAAA 169
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// LOCATION: 206, 227
// OTHER INFORMATION: n = A,T,C or G
US-09-814-353-17876
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APPLICANT: Warren, Wesley C.
APPLICANT: Warren, Wesley C.
APPLICANT: Tao, Nengbing
APPLICANT: Byat., John C.
TITLE OF INVENTION: WUCLEIC ACID AND OTHER MOLECULES ASSOCIATED WITH LACTATION AND
TITLE OF INVENTION: WUSCLE AND FAT DEPOSITION
TITLE OF INVENTION: WUSCLE AND FAT DEPOSITION
TITLE OF INVENTION: WUSCLE AND FAT DEPOSITION
TITLE OF INVENTION: WUSCLE AND FAT DEPOSITION
TITLE OF INVENTION: WORSER: USO/99/860,352
CURRENT FILING DATE: 2001-09-24
NUMBER OF SEQ ID NOS: 15112
LENGTH: 424
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Fublication No. US20030165831A1
GENERAL INFORMATION:
APPLICANT: Lie. John
APPLICANT: Lie. John
APPLICANT: Lille, Jamela
APPLICANT: Lille, Jamela
APPLICANT: Lille, Jamela
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APPLICANT: Lille, Jamela
APPLICANT: Lille, Jamela
APPLICANTON: THERAPY OF OVARIAN CANCER
FILE REFERENCE: MRI-006B
CURRENT APPLICATION NUMBER: US/09/814,353
CURRENT APPLICATION NUMBER: US 60/191,031
PRIOR FILING DATE: 2000-03-21
PRIOR FILING DATE: 2000-06-15
PRIOR PLICATION NUMBER: US 60/216,820
PRIOR PLILING DATE: 2000-06-15
PRIOR PLILING DATE: 2000-06-15
PRIOR PLILING DATE: 2000-06-15
PRIOR PLILING DATE: 2000-07-25
PRIOR PLILING DATE: 2000-07-25
PRIOR PLILING DATE: 2000-07-25
PRIOR PLILING DATE: 2000-07-25
PRIOR PLILING DATE: 2000-07-25
PRIOR PLILING DATE: 2000-12-21
NUMBER OF SEQ ID NOS: 22037
SOFTWARE: PRESEQ FOR Windows Version 4.0
SEQ ID NO 1753
LENGTH: 284
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ORGANISM: Bos taurus
OTHER INFORMATION: Clone ID: 48-LIB3058-026-Q1-K1-D12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 9.6%; Score 51; DB 13; Best Local Similarity 61.8%; Pred. No. 0.013; Matches 81; Conservative 0; Mismatches 50;
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Sequence 11218, Application US/09960352
Fatent No. US20020137139A1
GENERAL INFORMATION:
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US-09-814-353-17553
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TITLE OF INVENTION: Diagnosis of Diseases Associated with the Immune System by Determi
TITLE OF INVENTION: cytosine methylation
FILE REFERENCE: 5013.1014
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APPLICANT: Thompson, Pamela
APPLICANT: Thompson, Pamela
APPLICANT: Thompson, Pamela
APPLICANT: Thompson, Novel Genes, Compositions, Kits, AND METHODS FOR
TITLE OF INVENTION: IDENTIFICATION, ASSESSMENT, PREVENTION, AND
TITLE OF INVENTION: THERAPY OF OVARIAN CANCER
FILE REFERENCE: MRI-006B
CURRENT APPLICATION NUMBER: US/09/814,353
CURRENT APPLICATION NUMBER: US 60/191,031
PRIOR FILING DATE: 2000-03-21
PRIOR FILING DATE: 2000-03-21
PRIOR FILING DATE: 2000-05-25
PRIOR PLING DATE: 2000-05-25
PRIOR APPLICATION NUMBER: US 60/211,940
PRIOR PLING DATE: 2000-06-15
PRIOR PLING DATE: 2000-06-15
PRIOR PLING DATE: 2000-06-15
PRIOR PLING DATE: 2000-07-25
PRIOR PLING DATE: 2000-07-25
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PRIOR PLING DATE: 2000-07-25
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FEATURE:
NAME/KEY: misc_feature
LOCATION: 1, 98, 119, 145, 154, 170, 172, 193, 207, 212, 213, 214,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           .cn 9.0%; Score 47.4; DB 13; Length 113515; (1 Similarity 54.4%; Pred. No. 2; 93; Conservative 1; Mismarche.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              175 CCCTATCGGGTATATTTTGGAAGTTGTAAAATACTACRTGTTCTCTAA 225
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens) US-10-311-455-2148
                                                                                                 CURRENT PEPLICATION NUMBER: US/10/311,455
CURRENT FILING DATE: 2002-12-16
PRIOR APPLICATION NUMBER: PCT/EP01/07537
PRIOR FILING DATE: 2001-07-02
PRIOR FILING DATE: 2000-06-30
PRIOR PLING DATE: 2000-06-30
PRIOR PLING DATE: 2000-06-30
PRIOR FILING DATE: 2000-06-30
PRIOR FILING DATE: 2000-09-01
NUMBER OF SEQ 1D NOS: 2424
LENGTH: 113515
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 4872
LENGTH: 597
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                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: DNA
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
Matches 93; Conserv
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APPLICANT: Lillie, James
TITLE OF INVENTION: NOTEL GENES, COMPOSITIONS, KITS, AND METHODS FOR
TITLE OF INVENTION: IDENTIFICATION, ASSESSMENT, PREVENTION, AND
TITLE OF INVENTION: THERAPY OF OVARIAN CANCER
FILE REFERENCE: MRI-OGES
CURRENT APPLICATION NUMBER: US/09/814,353
CURRENT FILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: US 60/191,031
PRIOR APPLICATION NUMBER: US 60/207,124
PRIOR APPLICATION NUMBER: US 60/207,124
PRIOR APPLICATION NUMBER: US 60/211,940
PRIOR FILING DATE: 2000-05-25
PRIOR PILING DATE: 2000-06-15
PRIOR PILING DATE: 2000-06-15
PRIOR PILING DATE: 2000-07-07
PRIOR PILING DATE: 2000-07-07
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PRIOR FILING DATE: 2000-07-25
PRIOR FILING DATE: 2000-07-25
PRIOR FILING DATE: 2000-07-25
PRIOR FILING DATE: 2000-12-21
NUMBER OF SEQ ID NOS: 22037
SOFTWARE PRIOR PILING DATE: 2000-12-21
NUMBER OF SEQ ID NOS: 22037
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                                                          Length 424;
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                                                                                                               Indels
                                                       9.4%; Score 49.6; DB 10;
59.0%; Pred. No. 0.034;
Live 0; Mismatches 59;
                                                                                                                                                                       26 ATTTATATGCTGATTTATGGGTGATTTTGCTTCCTTCTT
                                                                                                                                                                                                                                                                                                                                                                                                  146 AAAGCAACGCTTGAAAAAAGGAAA 169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 10
US-09-814-353-16036/c
'Sequence 16036, Application US/09814353
; Publication No. US20030165831A1
; GENERAL INFORMATION:
; APPLICANT: Lee, John
                                                                                                                                                                                                                                                                                                                                                                                                                                                       72 AAAAAAAAACCAAAAAAAAAA 49
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 59.0
Matches 85; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-10-311-455-2148/c
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US-09-960-352-11218
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Sequence 1814, Application US/09960352

Ratent No. US20020137139A1

GRNERAL INFORMATION:
APPLICANT: Warren, Wesley C.
APPLICANT: Byatt, John C.
APPLICANT: Mathalagan, NUCLEIC ACID AND OTHER MOLECULES ASSOCIATED WITH LACTATION AND TITLE OF INVENTION: NUCLEIC ACID AND TITLE OF INVENTION: MUSCLE AND FAT DEPOSITION
FILE REFERENCE: 16511.006/37-21(10298)C
CURRENT APPLICATION NUMBER: US/09/960,352
CURRENT PILING DATE: 2001-09-24
NUMBER OF SEQ ID NOS: 15112
SEQ ID NO 8414
                                                                                                                                                                                                                                                                                                                                   81 CCCAAATTTTTCTTAAGCAAATATTTCTTTGCTAATCAATAAATTATCAAAAGAAAAAA 140
                                                                                                                                                                                                                                                                                               27 TITATATGCTGATTTATGGGTGATTTTGCTTCCTTCTTTATACTTTTATTTCCCAAA 86
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Publication No. US20030165831A1
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Lille, John
APPLICANT: Lille, James
TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS FOR TITLE OF INVENTION: IDENTIFICATION, ASSESSMENT, PREVENTION, AND TITLE OF INVENTION: THERAPY OF OVARIAN CANCER
FILE OF INVENTION: USER OF 1800 CURRENT APPLICATION NUMBER: US/09/814,353
CURRENT FILING DATE: 2001-03-21
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 8.8%; Score 46.6; DB 10; Length 312; Best Local Similarity 57.0%; Pred. No. 0.16; Matches 85; Conservative 0; Mismatches 64; Indels 0
                                                                                     Length 597;
                                                                                                                                    52; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: DNA (CRANTSM: BOB taurus ) ORGANTSM: BOB taurus ) ORGANTEM: INPORMATION: Clone ID: 36-LIB3058-048-Q1-K1-A8 US-09-960-352-8414
                                                                                Score 47.2; DB 13;
Pred. No. 0.16;
0; Mismatches 52;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; OTHER INFORMATION: n = A,T,C or US-09-814-353-11169
                                                                                Query Match
Best Local Similarity 59.4%;
Matches 76; Conservative
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Sequence 11169, Application US/09814353

Publication No. US20030165831A1

GENERAL INFORMATION:

APPLICANT: Lee, John

APPLICANT: Thompson, Pamela

APPLICANT: Thompson, Pamela

TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS FOR

TITLE OF INVENTION: THERAPY OF OVARIAN CANCER

TITLE OF INVENTION: THERAPY OF OVARIAN CANCER

FILE REFERENCE: MI-006B

CURRENT APPLICATION NUMBER: US 60/191,031

PRIOR PILING DATE: 2000-03-21

PRIOR PLING DATE: 2000-05-25

PRIOR APPLICATION NUMBER: US 60/207,124

PRIOR FILING DATE: 2000-06-15

PRIOR PILING DATE: 2000-06-15

PRIOR PILING DATE: 2000-07-07

PRIOR FILING DATE: 2000-07-07

PRIOR FILING DATE: 2000-07-25

PRIOR PILING DATE: 2000-07-25

PRIOR PILING DATE: 2000-07-27

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576, 577,
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                                                                                                                                                                                                                                                                                                                       Score 47.2; DB 13; Length 597;
Pred. No. 0.16;
0; Mismatches 52; Indels 0;
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575,
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571,
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521,
589
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516,
588,
                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 59.4%;
Matches 76; Conservative C
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421, 423, 440, 4
482, 508, 512, 5
578, 579, 580, 5
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LOCATION: 4
LOCATION: 4
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Sequence 2, Application US/10312841
Publication No. US20030186277A1
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Epigenomics AG
TITLE OF INVENTION: Diagnose von bedeutenden genetischen Parametern innerhalb des MHC
TITLE OF INVENTION: DIAGNOSE von bedeutenden genetischen Parametern innerhalb des MHC
CURRENT APPLICATION NUMBER: US/10/312,841
CURRENT FILING DATE: 2002-12-30
SEQ ID NOS: 2
SEQ ID NO 2
LENGTH: 3673778
                                                                                                                                                                                                              APPLICANT: Tao., Nengbirg
APPLICANT: Tao., Nengbirg
APPLICANT: Tao., Nengbirg
APPLICANT: Mathialagan, Magappan
APPLICANT: Mathialagan, Magappan
TITLE OF INVENTION: NUCLEIC ACID AND OTHER MOLECULES ASSOCIATED WITH LACTATION AND
TITLE OF INVENTION: MUSCLE AND FAT DEPOSITION
FILE REFERENCE: 15511.06(3)7-21(10298)C
CURRENT APPLICATION NUMBER: US/09/960,352
CURRENT PILLING DATE: 2001-09-24
NUMBER OF SEQ ID NOS: 15112
SEQ ID NO 8414
LENGTH: 312
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 3673778;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        63; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; TYPE: DNA
; ORGANISM: Bos taurus
; OTHER INFORMATION: CLone ID: 36-L/IB3058-048-Q1-K1-A8
US-09-960-352-8414
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 8.7%; Score 46.2; DB 10;
Best Local Similarity 57.1%; Pred. No. 0.2;
Matches 84; Conservative 0; Mismatches 63;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    8.7%; Score 46; DB 13;
57.7%; Pred. No. 25;
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                                                                                                                       Sequence 8414, Application US/09960352
Patent No. US20020137139A1
GENERAL INFORMATION:
APPLICANT: Warren, Wesley C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: DNA ORGANISM: Artificial Sequence
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Best Local Similarity
Matches 82; Conserv
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; LOCATION: (379615)
US-10-312-841-2
                                                                          RESULT 17
US-09-960-352-8414/c
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LY, NGCC
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DIAGNOSING AND MONITORING AUTOIMMUNE
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DIAGNOSING AND MONITORING AUTOIMMUNE
TITLE OF INVENTION: CHRONIC INFLAMMATORY DISEASES
FILE REFERENCE: 506612000120
CURRENT APPLICATION NUMBER: US/10/131,827
CURRENT PILING DATE: 2002-09-06
FRIOR PILING DATE: 2001-10-22
FRIOR PAPLICATION NUMBER: US 60/296,764
FRIOR FILING DATE: 2001-06-08
NUMBER OF SEQ ID NOS: 9090
SOFTWARE: PALENTIN VERSION 3.1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 480;
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Pred. No. 0.22;
0; Mismatches 46;
PRIOR APPLICATION NUMBER: US 60/191,031
PRIOR FILING DATE: 2000-03-21
PRIOR PAPLICATION NUMBER: US 60/207,124
PRIOR PAPLICATION NUMBER: US 60/211,940
PRIOR PILING DATE: 2000-06-15
PRIOR PELING DATE: 2000-07-07
PRIOR PELING DATE: 2000-07-07
PRIOR PELING DATE: 2000-07-07
PRIOR PELING DATE: 2000-07-07
PRIOR PELING DATE: 2000-07-25
PRIOR FILING DATE: 2000-07-25
PRIOR PELING DATE: 2000-12-21
                                                                                                                                                                                                                                                                                         NUMBER OF SEQ ID NOS: 22037
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 18006
LENCTH: 383
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Publication No. US20040009479A1
GENERAL INFORMATION:
APPLICANT: Wohlgemuth, Jay
APPLICANT: Fry, Kirk
APPLICANT: Wockward, Robert
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           sch 8.8%;
il Similarity 61.7%;
74; Conservative (
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US-09-814-353-18006
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CORGANISM: Homo sapiens
US-10-131-827-8192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
Matches 74; Conserv
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LENGTH: 480
                                                                                                                                                                                                                                                                                                                                                                                             TYPE: DNA
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127 TCAAAAGAAAAAAAACTGAAAGCAACGCTTGAAAAAAGGAAAGTTAGCCCTATCGGGTA 186
       67 TACTITIATITIATICCCAAATITITICTIAAGCAAATATITICTITIGCTAATCAATAA 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          187 TATTITIGGAAGTIGTAAAATACTACRIGTICTCTTCTAAGTCCCACTCCTCTGTTTTCTT 246
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NAME/KEY: misc_feature
LOCATION: 57, 58, 59, 60, 100, 102, 128, 129, 130, 131, 132, 133, 137,
LOCATION: 57, 58, 59, 60, 100, 102, 128, 129, 130, 131, 132, 133, 137,
LOCATION: 138, 141, 142, 143, 150, 174, 176, 177, 184, 185, 190,
LOCATION: 198, 199, 208, 209, 210, 211, 212, 213, 219, 222, 232, 234,
LOCATION: 249, 252, 253, 254, 263, 264, 265, 268, 269, 276
OTHER INFORMATION: n = A,T,C or G
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351,
408,
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SEQUENCE 11146, Application US/09814353

Publication No. US20030165831A1

REBEREL INPORMATION:

APPLICANT: Thompson, Pamela

APPLICANT: Thompson, Pamela

APPLICANT: Thillie, James

ITILE OF INVENTION: IDENTIFICATION, ASSESSMENT, PREVENTION, AND

ITILE OF INVENTION: IDENTIFICATION, ASSESSMENT, PREVENTION, AND

ITILE OF INVENTION: IDENTIFICATION, ASSESSMENT, PREVENTION, AND

ITILE OF INVENTION: IDENTIFICATION, ASSESSMENT, PREVENTION, AND

ITILE OF INVENTION: IDENTIFICATION, ASSESSMENT, PREVENTION, AND

ITILE OF INVENTION: IDENTIFICATION, ASSESSMENT, PREVENTION, AND

ITILE OF INVENTION: WIMBER: US 60/201, 031

PRIOR FILING DATE: 2000-03-21

PRIOR FILING DATE: 2000-06-15

PRIOR FILING DATE: 2000-06-15

PRIOR FILING DATE: 2000-07-07

PRIOR FILING DATE: 2000-07-07

PRIOR FILING DATE: 2000-07-07

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PRIOR FILING DATE: 2000-07-07

PRIOR FILING DATE: 2000-07-07

PRIOR FILING DATE: 2000-07-07

SOFTWARE: FASESED TO NOS: 22037, 672

NUMBER OF SEQ ID NOS: 22037, 1446

LINGTH. 4614
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349,
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433,
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340,
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LOCATION: 284, 286, 294, 295, 296,
LOCATION: 313, 314, 325, 335,
LOCATION: 359, 367, 335,
LOCATION: 409, 413, 414, 424, 426,
LOCATION: n = A,T,C or G
                                                                                                                                                                                    206 TTINNNNNAÄÄÄÄÄÄÄÄÄÄ
                                                                                                                247 TGAGCAGGAAAGAGAAAG 264
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APPLICANT: Lee, John
APPLICANT: Lee, John
APPLICANT: Lille, Jamela
APPLICANT: Lille, Jamela
APPLICANT: Lille, Jamela
APPLICANT: Lille, Jamela
TITLE OF INVENTION: IDENTIFICATION, ASSESSMENT, PREVENTION, AND
TITLE OF INVENTION: IDENTIFICATION, ASSESSMENT, PREVENTION, AND
TITLE OF INVENTION: IDENTIFICATION, ASSESSMENT, PREVENTION, AND
TITLE OF INVENTION: IDENTIFICATION CANCER
FILE REFERENCE: MRI-066B
CURRENT FILING DATE: 2001-03-21
PRIOR PLILOG DATE: 2000-03-21
PRIOR FILING DATE: 2000-05-25
PRIOR PLILOG DATE: 2000-06-15
PRIOR PLILOG DATE: 2000-06-15
PRIOR PLILOG DATE: 2000-06-15
PRIOR PLILOG DATE: 2000-07-07
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PRIOR PLILOG DATE: 2000-07-07
PRIOR PLILOG DATE: 2000-07-07
PRIOR PLILOG DATE: 2000-11-01
NUMBER OF SEQ ID NOS: 22037
SOFTWARE: FRATESQ for Windows Version 4.0
SEQ ID NO 4849
LENGTH: 463
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LOCATION: 57, 59, 59, 60, 100, 102, 128, 129, 130, 131, 132, 133, 137,
LOCATION: 138, 140, 141, 142, 143, 150, 174, 177, 184, 185, 130,
LOCATION: 138, 140, 141, 142, 143, 150, 174, 177, 184, 185, 130,
LOCATION: 249, 252, 253, 254, 263, 264, 265, 268, 269, 276
OTHER INFORMATION: n = A,T,C or G
FEATURE:
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| NAME/KEY: misc_feature
| LOCATION: 439, 440, 441, 442, 444, 447, 451
| JOHEN INPORMATION: n = A,T,C or G
| US-09-814-353-4849
                                                                                                                                                                     88140 AACAAATAAACACGTAAACAAA 88119
                                                                                                                                                                                                                                                                                                                                                             ; Sequence 4849, Application US/09814353; Publication No. US20030165831A1; GENERAL INFORMATION:
                                                                                                             CTGAAAGCAACGCTTGAAAAA 164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                          RESULT 19
US-09-814-353-4849
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Thompson, Pamela
APPLICANT: Lillie, James
TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS FOR
TITLE OF INVENTION: LDERAPY OF OVARIAN CANCER
FILE REFERENCE: MRI-1006B
CURRENT APPLICATION NUMBER: US/09/814,353
CURRENT FILING DATE: 2001-03-21
                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 8.6%; Score 45.6; DB 13; Length 406; Best Local Similarity 56.2%; Pred. No. 0.32; Aatches 81; Conservative 0; Mismatches 63; Indels 0
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8.5%; Score 45; DB 13; Length 35
Best Local Similarity 53.0%; Pred. No. 0.42;
Matches 96; Conservative 0; Mismatches 85; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            26 ATTTATATGCTGATTTATGGGTGATTTTGCTTCCTTCTTTATACTTT
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PRIOR FILLING DATE: 2000-03-21

PRIOR FILLING DATE: 2000-03-21

PRIOR FILLING DATE: 2000-05-25

PRIOR PILLING DATE: 2000-05-25

PRIOR PILLING DATE: 2000-05-15

PRIOR APPLICATION NUMBER: US 60/211,940

PRIOR PILLING DATE: 2000-06-15

PRIOR PELING DATE: 2000-06-15

PRIOR PELING DATE: 2000-07-07

PRIOR PILLING DATE: 2000-07-25

PRIOR PILLING DATE: 2000-07-25

PRIOR PILLING DATE: 2000-07-25

PRIOR PILLING DATE: 2000-07-25

PRIOR PILLING DATE: 2000-07-25

PRIOR PILLING DATE: 2000-12-21

NUMBER OF SEQ ID NOS: 22037

SOFTWARE: FREESEQ FOR WINDOWS VERSION 4.0

SEQ ID NO 17359
PRIOR APPLICATION NUMBER: US 60/220,661
PRIOR FILING DATE: 2000-07-25
PRIOR PILING DATE: 2000-12-21
NUMBER OF SEQ ID NOS: 22037
SOFTWARE: PastSEQ for Windows Version 4.0
EROUTH: 406
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Publication No. US20030165831A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                        FEATURE:

| NAME/KEY: misc feature

| LOCATION: 225, 226, 227, 228

| OTHER INFORMATION: n = A,T,C or G

| US-09-814-353-17782
                                                                                                                                                                                                                           TYPE: DNA ORGANISM: Homo sapiens
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ORGANISM: Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-09-814-353-17359
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                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Epigenomics AG
TITLE OF INVENTION: Diagnose von bedeutenden genetischen Parametern innerhalb des MHC
FILE REPERENCE: E01/1208/WO
CURRENT PELLATION VMDER: US/10/312,841
CURRENT FILING DATE: 2002-12-30
NUMBER OF SEQ ID NOS: 2
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     146 TITINGGGGAAAAAAAAAAAAAAAAAAANCNNTITITINNCCCCCCCCCNATITIT 205
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US-09-814-353-17782/C
; Sequence 17782, Application US/09814353
; Publication No. US20030165831A1
; GENERAL INFORMATION:
; APPLICANT: Lee, John
; APPLICANT: Lee, John
; APPLICANT: Lillie, James
; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS FOR
; TITLE OF INVENTION: THERAPY OF OVARIAN CANCER
; TITLE OF INVENTION: THERAPY OF OVARIAN CANCER
; TITLE OF INVENTION: USBENTIFICATION, ASSESSMENT, PREVENTION, AND
; TITLE OF INVENTION: USBENT: US/09/814,353
; CURRENT FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: US 60/191,031
; PRIOR PELING DATE: 2000-05-25
; PRIOR FILING DATE: 2000-05-25
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: US 60/201,124
; PRIOR PELING DATE: 2000-06-15
; PRIOR FILING DATE: 2000-06-15
; PRIOR FILING DATE: 2000-06-15
; PRIOR FILING DATE: 2000-07-07
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
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51.2%; Pred. No. 28;
ive 1; Mismatches
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                                                                                                                                                                                                                                                                              Sequence 1, Application US/10312841; Publication No. US20030186277A1; GENERAL INFORMATION:
                                                                                        247 TGAGCAGGAAAGAGAAG 264
                                                                                                                                           206 TTNNNNNNAAAAAAAAKG 223
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: DNA ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ilarity 51.2%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Best Local Similarity
Matches 104; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; NAME/KEY: unsure
; LOCATION: (3294164)
US-10-312-841-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LENGTH: 3673778
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                                                                                                                                      149 rirrinaanirrrrrrirrirrrigaaratarirrrrrrrrrarranaaaararrarr 208
                                                                                                                                                                                                       132 AGAAAAAAAAACTGAAAGCAACGCTTGAAAAAGGAAAGTTAGCCCTATCGGGTATATTT 191
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8.5%; Score 44.8; DB 13;
Best Local Similarity 61.4%; Pred. No. 0.44;
Matches 70; Conservative 0; Mismatches 44;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   | FEATURE:
| NAME/KEY: misc_feature
| LOCATION: 1266, 227
| OTHER INFORMATION: n = A,T,C or G
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US-09-814-353-17876/c
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Sequence 4726, Application US/09814353 Publication No. US20030165831A1 GENERAL INFORMATION: APPLICANT: Lee, John APPLICANT: Thompson, Pamela

RESULT 25 US-09-814-353-4726/c

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49 ATTITIGCTICCTICTITATACTTTATITITATICCCAAATTTTTCTTAAGCAAATATTTCT 108
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           109 TIGCTAATCAATAATTATCAAAAGAAAAAAAAAACTGAAAGCAACGCTTGAAAAAAGGAA 168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS FOR TITLE OF INVENTION: IDENTIFICATION, ASSESSMENT, PREVENTION, AND TITLE OF INVENTION: IDENTIFICATION, ASSESSMENT, PREVENTION, AND TITLE OF INVENTION: THERAPY OF OVARIAN CANCER FILE OF INVENTION: THERAPY OF OVARIAN CANCER FILE OF INVENTION: THERAPY OF OVARIAN CANCER FILE OF THE METOGEN GOOD TO STATE TO SOUL 03-21

PRIOR FILING DATE: 2001-03-21

PRIOR FILING DATE: 2000-03-21

PRIOR FILING DATE: 2000-03-21

PRIOR FILING DATE: 2000-05-25

PRIOR PAPLICATION NUMBER: US 60/216,820

PRIOR PALICATION NUMBER: US 60/216,820

PRIOR FILING DATE: 2000-07-07

PRIOR FILING DATE: 2000-07-07

PRIOR FILING DATE: 2000-07-21

PRIOR FILING DATE: 2000-07-25

PRIOR PELICATION NUMBER: US 60/257,672

PRIOR FILING DATE: 2000-07-25

PRIOR PELICATION NUMBER: US 60/257,672

PRIOR FILING DATE: 2000-07-25

PRIOR PELICATION NUMBER: US 60/257,672

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PRIOR PELICATION NUMBER: US 60/257,672
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FEATURE:
NAME/KEY: misc feature
LOCATION: 666, 681, 689, 690, 692, 694, 695, 696, 697, 698, 699, 700,
LOCATION: 701, 703, 704, 706, 711, 713, 714
COTHER INFORMATION: n = A,T,C or G
US-09-814-353-4726
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Eublication No. US20030165831A1
GENERAL INFORMATION:
APPLICANT: Lee, John
APPLICANT: Thompson, Pamela
APPLICANT: Lilie, James
ITILE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS FOR
TITLE OF INVENTION: IDENTIFICATION, ASSESSMENT, PREVENTION, AND
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8.5%; Score 44.8; DB 13;
Best Local Similarity 57.9%; Pred. No. 0.67;
Matches 70; Conservative 0; Mismatches 51;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 26
US-09-814-353-11024/C
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ORGANISM: Homo sapiens
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US-09-834-975-451
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            109 TTGCTAATCAATTATCAAAAGAAAAAAAAAAACTGAAAGCAACGCTTGAAAAAAGGAA 168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     191 AANTTITITITITITITITICCCNCNTITITITITAANAATTITITINNAAAAAAATNITITI 132
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LOCATION: 56, 57, 59, 137, 147, 148, 156, 162, 167, 169, 173, 189, LOCATION: 200, 202, 214, 223, 225, 227, 231, 239, 240, 248, 257, 259, LOCATION: 260, 266, 270, 273, 274, 275, 277, 278, 280, 283, 287, 295, LOCATION: 306, 311, 313, 317, 340, 344, 351, 353, 361, 367, 370 OTHER INFORMATION: n = A,T,C or G
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           694, 695, 696, 697, 698, 699, 700,
713, 714
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| Publication No. US20030165831A1
| GENERAL INFORMATION:
| APPLICANT: Lee, John Pamela
| APPLICANT: Linie, James
| TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS FOR TITLE OF INVENTION: THERAPY OF OVARIAN CANCER; TITLE FERENCE: MEI-0068
| TITLE FERENCE: MEI-0068
| CURRENT APPLICATION NUMBER: US/09/814,353
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8.5%; Score 44.8; DB 13; Length 723;
Best Local Similarity 57.9%; Pred. No. 0.67;
Matches 70; Conservative 0; Mismatches 51; Indels 0
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581,
645,
THERAPY OF OVARIAN CANCER
           TITLE REFERENCE: WRI-OGE
CURRENT APPLICATION NUMBER: US/09/814,353
CURRENT FILING DATE: 2001-03-21
PRIOR PILING DATE: 2000-03-21
PRIOR PILING DATE: 2000-03-21
PRIOR FILING DATE: 2000-05-25
PRIOR PILING DATE: 2000-05-25
PRIOR APPLICATION NUMBER: US 60/201,940
PRIOR PILING DATE: 2000-05-25
PRIOR PILING DATE: 2000-05-25
PRIOR PILING DATE: 2000-05-15
PRIOR PILING DATE: 2000-07-07
PRIOR PILING DATE: 2000-07-07
PRIOR PILING DATE: 2000-07-07
PRIOR PRIOR DATE: 2000-07-07
PRIOR PILING DATE: 2000-07-25
PRIOR APPLICATION NUMBER: US 60/257,672
PRIOR PILING DATE: 2000-07-25
PRIOR PILING DATE: 2000-07-25
PRIOR PILING DATE: 2000-07-25
PRIOR PILING DATE: 2000-07-21
NUMBER OF SEQ ID NOS: 22037
SOFTWARE: PASSES OF WINDOWS VERSION 4.0
SEQ ID NO 11024
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LOCATION: 371, 378, 379, 381, 400, LOCATION: 434, 475, 476, 479, 480, LOCATION: 528, 529, 533, 535, 536, LOCATION: 593, 597, 603, 615, 618, OTHER INFORMATION: n = A,T,C or G
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FEATURE:
NAME/KEY: misc_feature
LOCATION: 686, 689, 689, 690, 692,
LOCATION: 701, 703, 704, 706, 711,
OTHER INFORMATION: n = A,T,C or G
US-09-814-353-11024
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME/KEY: misc feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              misc_feature
  OF INVENTION:
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Sequence 451, Application US/09834975

Sequence 451, Application US/09834975

Patent No. US20020110815A1

GENERAL INFORMATION

APPLICANT: Brown, Jeffrey

APPLICANT: Blow, Andrew

APPLICANT: Bolt, Andrew

APPLICANT: Bolt, Andrew

TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS AND METHODS

TITLE OF INVENTION: OF HUMAN CANCERS

TITLE OF INVENTION: OF HUMAN CANCERS

TITLE OF INVENTION: OF HUMAN CANCERS

CURRENT APPLICATION NUMBER: US/09/834,975

CURRENT FILING DATE: 2001-04-13

PRIOR FILING DATE: 2000-04-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  45 GGTGATTTTGCTTCCTTCTTTATACTTTTATTTCCCAAATTTTTCTTAAGCAAATAT
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8.4%; Score 44.4; DB 10;
Best Local Similarity 54.9%; Pred. No. 0.64;
Matches 84; Conservative 0; Mismatches 69;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                51;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 8.4%; Score 44.4; DB Best Local Similarity 59.5%; Pred. No. 0.47; Matches 75; Conservative 0; Mismatches
PRIOR APPLICATION NUMBER: US 60/191,031
PRIOR PILING DATE: 2000-03-21
PRIOR PILING DATE: 2000-03-21
PRIOR PILING DATE: 2000-05-25
PRIOR PILING DATE: 2000-05-25
PRIOR PILING DATE: 2000-06-15
PRIOR PILING DATE: 2000-06-15
PRIOR PILING DATE: 2000-07-07
PRIOR PILING DATE: 2000-07-07
PRIOR PILING DATE: 2000-07-07
PRIOR APPLICATION NUMBER: US 60/226,661
PRIOR PILING DATE: 2000-07-25
PRIOR PILING DATE: 2000-07-25
PRIOR PILING DATE: 2000-12-21
NUMBER OF SEX ID NOS: 22037
SOFTWARE: PRESEX for Windows Version 4.0
SECTIVATED: 228
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SCOTTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 451
LENGTH: 425
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NAME/KEY: misc_feature
LOCATION: (1)...(425)
OTHER INFORMATION: n = A,T,C or G
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Sequence 66, Application US/10055098

Publication No. US200301399541

GENERAL INFORMATION:

APPLICANT: Rosen et al.

TITLE OF INVENTION: 49 Human Secreted Proteins
FILE REFERENCE: PZ032P1

CURRENT APPLICATION NUMBER: US/10/055,098

CURRENT FILING DATE: EARLIER FILING DATE: 1000-02-23

PRIOR FILING DATE: EARLIER FILING DATE: 1999-08-24

PRIOR FILING DATE: EARLIER FILING DATE: 1999-08-24

PRIOR FILING DATE: EARLIER FILING DATE: 1999-08-24

PRIOR PRICATION NUMBER: EARLIER APPLICATION NUMBER: 60/097,917

PRIOR PLING DATE: EARLIER FILING DATE: 1999-08-25

PRIOR PLING DATE: EARLIER FILING DATE: 1999-08-25

PRIOR FILING DATE: EARLIER FILING DATE: 1999-08-25

PRIOR FILING DATE: EARLIER FILING DATE: 1999-08-25

PRIOR FILING DATE: EARLIER FILING DATE: 1999-08-31

NUMBER OF SEQ ID NOS: 170

SOFTWARE: PATENTING DATE: EARLIER FILING DATE: 1999-08-31

NUMBER OF SEQ ID NOS: 170

SEQ ID NO 66

LENGTH: 664
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       147 AAGCAACGCTTGAAAAAAGGAAAGTTAGCCCTATCGGGTATATTTTGGAAGTTGTA 202
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              8.4%; Score 44.4; DB 9; Length 664; 52.8%; Pred. No. 0.8; tive 1; Mismatches 82; Indels
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Pred. No. 0.8;
1; Mismatches 82;
                                                                                                                                                                                                                                                    PEATURE:
| NAME/KEY: SITE
| LOCATION: (31)
| OTHER INFORMATION: n equals a,t,g, or c
| NAME/KEY: SITE
| LOCATION: (63)
| OTHER INFORMATION: n equals a,t,g, or c
| US-09-904-615-66
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) OTHER INFORMATION: n equals a,t,g, or c
US-10-055-098-66
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              PRIOR APPLICATION NUMBER: 60/097,917
PRIOR FILING DATE: 1998-08-25
PRIOR APPLICATION NUMBER: 60/098,634
PRIOR FILING DATE: 1998-08-31
NUMBER OF SEC ID NOS: 170
SOFTWARE: PALENTIN Ver. 2.0
SEC ID NO 66
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Best Local Similarity 52.8%;
Matches 93; Conservative
FILING DATE: 2000-02-23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 52.81
Matches 93; Conservative
                                                                                                                                                                                                          TYPE: DNA ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: DNA ORGANISM: Homo sapiens
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NAME/KEY: SITE
LOCATION: (31)
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521 AAAAACCTCACAATAATATAAATTTTTACACTATGAAGTACACATTGGAATTTGAA 466
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                                                                                                                                                                                                                                                                                      Sequence 66, Application US/09739254
; Patent No. US20010021700A1
; GENERAL INFORMATION:
APPLICANT: Rosen et al.
TILE OF INVENTION: 49 Human Secreted Proteins
FILE REFERENCE: PZ032P1
CURRENT APPLICATION NUMBER: US/09/739, 254
CURRENT FILING DATE: 2000-12-19
; EARLIER FILING DATE: 2000-02-23
; EARLIER FILING DATE: 1999-08-24
; EARLIER FILING DATE: 1999-08-24
; EARLIER FILING DATE: 1999-08-24
; EARLIER FILING DATE: 1999-08-25
; EARLIER FILING DATE: 1999-08-25
; EARLIER FILING DATE: 1998-08-15
; NUMBER OF SEQ ID NOS: 170
; SOFTWARE: PatentIn Ver: 2.0
; SEQ ID NO 66
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8.4%; Score 44.4; DB 9;
Best Local Similarity 52.8%; Pred. No. 0.8;
Matches 93; Conservative 1; Mismatches 82;
                                                                                                                                      147 AAGCAACGCTTGAAAAAGGAAAGTTAGCCCTA 179
                                                                                                                                                                                  131 AAAAAAAAAAAAAAAAAAAAATTTCCCCCA 163
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Patent No. US20020026040A1
GENERAL INFORMATION:
APPLICANT: ROSEN et al.
TITLE OF INVENTION: 49 Human Secreted Proteins
FILE REFERENCE: PZ03ZP1
CURRENT PAPLICATION NUMBER: US/09/904,615
CURRENT FILING DATE: 2001-07-16
PRIOR APPLICATION NUMBER: 09/511,554
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; LOCATION: (63)
; OTHER INFORMATION: n equals a,t,g, or
US-09-739-254-66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LOCATION: (31)
OTHER INFORMATION: n equals a,t,g,
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ORGANISM: Homo sapiens
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US-09-904-615-66/c
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Sequence 1, Application US/10312841

Publication No. US20030186277A1

GENERAL INFORMATION:

APPLICANT: Epigenomics AG

TITLE OF INVENTION: Diagnose von bedeutenden genetischen Parametern innerhalb des MHC

FILE REFERENCE: E01/1208/WO

CURRENT APPLICATION WUMBER: US/10/312,841

CURRENT FILING DATE: 2002-12-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       686898 ТГТТАТТААТАТТТТАТСАТТАААТТАТАТТТТТАТАТТТТСАСАТАААТАААААТТА 686957
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            4434 AAAAAAAAAAAAACATATTAAAACAAACTCTTCAATAATTATATCTTAAATACCTTTTT 4375
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        65 TATACTTTTATTTATTCCCAAATTTTTCTTAAGCAAATATTTCTTTGCTAATCAATAAAT 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             125 TATCAAAAGAAAAAAAACTGAAAGCAACGCTTGAAAAAGGAAAGTTAGCCCTATCGGG 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   137 AAAAAACTGAAAGGAACGCTTGAAAAAAGGAAAGTTAGCCCTATCGGGTATATTTTGGAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              77 TATTCCCAAATTTTTCTTAAGCAAATATTTCTTTGCTAATCAATAAATTATCAAAAGAAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         17 TCGTGGCTGATTTATATGCTGATTTATGGGTGATTTTGCTTCCTTTTATACTTTTATT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 13; Length 3673778;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens) US-10-311-455-1110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      185 TATATTTTGGAAGTTGTAAAATACTACRTGTTCTCTTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
8.4%; Score 44.4; DB 13;
Best Local Similarity 54.4%; Pred. No. 2.5;
Matches 87; Conservative 1; Mismatches 72;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            93;
TITLE OF INVENTION: cytosine methylation
FILE REFERENCE: 5013.1014
CURRENT APPLICATION NUMBER: US/10/311,455
CURRENT FILING DATE: 2002-12-16
FRICR APPLICATION NUMBER: PCT/EP01/07537
FRICR FILING DATE: 2001-07-02
FRICR FILING DATE: 2000-06-30
FRICR FILING DATE: 2000-06-30
FRICR FILING DATE: 2000-06-30
FRICR FILING DATE: 2000-06-30
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FRICR FILING DATE: 2000-06-30
FRICR FILING DATE: 2000-06-30
FRICR FILING DATE: 2000-06-30
FRICR FILING DATE: 2000-09-01
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Pred. No. 68;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: DNA ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 51.8%;
Matches 100; Conservative (
                                                                                                                                                                                                                                                                                                                                                                                                                                              ORGANISM: Artificial Sequence
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; LOCATION: (3294164)
US-10-312-841-1
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Sequence 1110, Application US/10311455

Publication No. US20030143606A1

GENERAL INFORMATION:

APPLICANT: OLEK, Alexander

APPLICANT: PIEPENBROCK, Christian

APPLICANT: BERLIN, Kurt

TITLE OF INVENTION: Diagnosis of Diseases Associated with the Immune System by Determ
                                                                                                                                                                 TITATATGCIGATITATGGGIGATITIGCTICCTICTITATACTITIATTTCCCAAA 86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TITATATGCTGATTTATGGGTGATTTTGCTTCCTTTTATATTTTATTTTATTCCCAAA 86
                                                                                                                                                                                                                                                                                      147 AAGCAACGCTTGAAAAAGGAAAGTTAGCCCTATCGGGTATATTTTGGAAGTTGTA 202
                                                                                                                                                                                                                                                                                                                                               AAAAACCTCACAATAATATAAATTTTTACACTATGAAGTACACATTGGAATTTGAA 466
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      521 AAAAACCTCACAATAATATAAATTTTTACACTATGAAGTACACATTGGAATTTGAA 466
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             147 AAGCAACGCTTGAAAAAGGAAAGTTAGCCCTATCGGGTATATTTTGGAAGTTGTA 202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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Pred. No. 0.8;
1; Mismatches 82; Indels 0.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION AND ADDRESS OF TITLE OF INVENTION: 49 Human Secreted Proteins FILE REFERENCE: P2032P1
CURRENT APPLICATION NUMBER: US/10/054,988
CURRENT FILING DATE: 2002-01-25
FRICH APPLICATION NUMBER: 09/914,615
FRICH APPLICATION NUMBER: 09/511,554
FRICH APPLICATION NUMBER: 09/511,554
FRICH APPLICATION NUMBER: 00/097,917
FRICH APPLICATION NUMBER: 60/097,917
FRICH APPLICATION NUMBER: 60/097,917
FRICH APPLICATION NUMBER: 60/097,917
FRICH APPLICATION NUMBER: 60/098,634
FRICH APPLICATION NUMBER: 60/098,634
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FRICH APPLICATION NUMBER: 60/098,634
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OTHER INFORMATION: n equals a,t,g, or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LOCATION: (63)
COTHER INFORMATION: n equals a,t,g, or US-10-054-988-66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 66, Application US/10054988; Publication No. US20030087341A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 52.8%;
Matches 93; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-10-054-988-66/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME/KEY: SITE
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us-10-027-632-1.rnpb

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PRIOR FILING DATE: 2001-07-18
NUMBER OF SEQ ID NOS: 14084
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 8434
                                                                                                             TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FEATURE:
NAME/KEY: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
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                                                                                                                                                                                                                   GENERAL INFORMATION:
APPLICANT: Lee, John
APPLICANT: Lee, John
APPLICANT: Thompson, Pamela
APPLICANT: Thompson, Pamela
APPLICANT: Thompson, Pamela
APPLICANT: Lillie, James
TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS FOR
TITLE OF INVENTION: THERAPY OF OVARIAN CANCER
TITLE OF INVENTION: THERAPY OF OVARIAN CANCER
TITLE OF INVENTION: UNBER: US/09/814,353
CURRENT FILING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: US 60/191,031
PRIOR APPLICATION NUMBER: US 60/207,124
PRIOR PLING DATE: 2000-05-25
PRIOR PLING DATE: 2000-05-25
PRIOR PLING DATE: 2000-07-07
PRIOR PLING DATE: 2000-07-07
PRIOR PLING DATE: 2000-07-07
PRIOR PLING DATE: 2000-07-07
PRIOR PLING DATE: 2000-07-25
PRIOR PLING DATE: 2000-07-25
PRIOR PLING DATE: 2000-07-25
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PRIOR PLING DATE: 2000-07-25
PRIOR PLING DATE: 2000-07-25
PRIOR PLING DATE: 2000-07-27
PRIOR PLING DATE: 2000-07-27
PRIOR PLING DATE: 2000-07-27
PRIOR PLING DATE: 2000-07-27
PRIOR PLING DATE: 2000-12-21
NUMBER OF SEQ ID NOS: 22037
PROFTWARE PARESEQ FOR WINGOWS VERSION 4.0
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| Publication No. US2003009974A1
| GENERAL INFORMATION:
| GENERAL INFORMATION:
| APPLICANT: Lillie, James
| APPLICANT: Wangy Youzhen
| TITLE OF INVENTION: FOR IDENTIFICATIONS, KITS, AND
| TITLE OF INVENTION: THERRY OF BREAST CANCER
| FILE REFERENCE: MILLIANTON THERRY OF BREAST CANCER
| FILE REFERENCE: MILLIANTON UNMBER: US/10/198,846
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 44; DB 13
Pred. No. 0.65;
0; Mismatches
                                                                                                                                                                                 Sequence 17383, Application US/09814353
Publication No. US20030165831A1
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PRIOR APPLICATION NUMBER: 60/306,220
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                                                            687018 ATTTAAAATAT 687030
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Best Local Similarity 57.1%;
Matches 80; Conservative
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US-10-198-846-8434
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D AND OTHER MOLECULES ASSOCIATED WITH LACTATION AND
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                                                                                                                                                                                                                                                                                                                                                               533,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 600;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       8.3%; Score 44; DB 15; Length 60
48.7%; Pred. No. 0.96;
tive 0; Mismatches 100; Indele
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; TYPE: DNA
; ORGANISM: Bos taurus
; OTHER INFORMATION: Clone ID: 52-LIB3058-016-Q1-K1-E12
US-09-960-352-12183
                                                                                                                                                                                                                                                                                                                                                            527,
563,
599
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Patent No. US20020137139A1
GRENERAL INFORMATION:
APPLICANT: Wateren, Wealey C.
APPLICANT: Byatt, John C.
APPLICANT: Byatt, John C.
APPLICANT: Byatt, John C.
TITLE OF INVENTION: MUSCLE AND FAT DEPOSITION
TITLE OF INVENTION: MUSCLE AND FAT DEPOSITION
FILE REFERENCE: 15511.006/37-21(10298)C
CURRENT APPLICATION NUMBER: US/09/960,352
CURRENT FILING DATE: 2001-09-24
NUMBER OF SEQ ID NOS: 15112
LENGTH: 236
                                                                                                                                                                                                                                                                                                                                                               526,
562,
598,
                                                                                                                                                                                                                                                                                                                                                               524,
561,
594,
NAME/KEY: misc_feature
LOCATION: 2, 14, 27, 61, 150, 153,
LOCATION: 229, 230, 232, 234, 236,
LOCATION: 323, 324, 325, 326, 328,
LOCATION: 346, 349, 350, 351, 352,
OTHER INFORMATION: n = A,T,C or G
                                                                                                                                                                                                                                                                                                                            ; NAME/KEY: misc_feature
; LOCATION: 518, 519, 520, 521, 522,
; LOCATION: 536, 537, 538, 541, 559,
; LOCATION: 570, 575, 589, 590, 592,
; OTHER INFORMATION: n = A,T,C or G
US-10-198-846-8434
                                                                                                                                                                                      LOCATION: 374, 375, 376, 377, 379, LOCATION: 401, 402, 403, 404, 406, LOCATION: 427, 435, 436, 437, 437, 437, LOCATION: 479, 480, 481, 483, OTHER INFORMATION: n = A,T,C or G
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Best Local Similarity 48.7*
Matches 95; Conservative
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FEATURE
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                                      Gaps
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APPLICANT: Thompson, Pamela
APPLICANT: Thompson, Pamela
APPLICANT: Lillie, James
TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS FOR
TITLE OF INVENTION: IDENTIFICATION, ASSESSMENT, PREVENTION, AND
TITLE OF INVENTION: THERAPY OF OVARIAN CANCER
TITLE OF INVENTION: THERAPY OF OVARIAN CANCER
TITLE OF INVENTION: THERAPY OF OVARIAN CANCER
CURRENT FILING DATE: 2001-03-21
FRIOR APPLICATION NUMBER: US 60/191,031
FRIOR PELLING DATE: 2000-03-21
FRIOR PELLING DATE: 2000-05-25
FRIOR PELLING DATE: 2000-06-15
FRIOR PELLING DATE: 2000-06-15
FRIOR PELLING DATE: 2000-07-07
FRIOR PELLING DATE: 2000-07-07
FRIOR PELLING DATE: 2000-07-25
FRIOR PELLING DATE: 2000-07-25
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0.67;
--hes 62; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       62; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              8.3%; Score 43.8; DB 13; 56.6%; Pred. No. 0.73;
                                   0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0; Mismatches
        Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 17383, Application US/09814353
Publication No. US20030165831A1
GENERAL INFORMATION:
APPLICANT: Lee, John
APPLICANT: Thompson, Pamela
                                                                                                                                                                                                                                                                                                                       147 AAGCAACGCTTGAAAAAAGGAAA 169
                                                                                                                                                                                                                                                                                                                                                                                167 AATGTTAĞTGTĞAAATGACAAA 189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAGCAACGCTTGAAAAAAGGAAA 169
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  56.6%;
     Best Local Similarity 56.6
Matches 81; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       81; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 38
US-09-814-353-17383/c
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US-09-814-353-5380
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Best Local (
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Sequence 5380, Application US/09814353; Publication No. US20030165831A1
GENERAL INFORMATION:
APPLICANT: Lee, John

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       333
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NAME/KRY: misc_feature
NAME/KRY: misc_feature
CATION: 224, 225, 238, 245, 248, 255, 257, 258, 260, 261, 269, 276, 10CATION: 277, 278, 279, 280, 289, 292, 293, 302, 308, 322, 330, 335, 10CATION: 347, 346, 348, 349, 350, 353, 366, 367, 371, 377, 384, 10CATION: 385, 398, 408, 422, 423, 440, 452, 453, 454, 455, 456
OTHER INFORMATION: n = A,T,C or G
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LOCATION: 128, 127, 128, 131, 132, 134, 150, 112, 114, 120, 121, LOCATION: 152, 127, 128, 131, 132, 134, 150, 151, 152, 153, 154, LOCATION: 152, 156, 157, 158, 159, 160, 161, 162, 163, 183, 184, 186, LOCATION: 188, 189, 190, 192, 193, 195, 196, 197, 209, 221, 223 OTHER INFORMATION: n = A,T,C or G
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550, 554, 568,
APPLICANT: Lillie, James
APPLICANT: Lillie, James
TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS FOR
TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS FOR
TITLE OF INVENTION: THERAPY OF OVARIAN CANCER
TITLE OF INVENTION: THERAPY OF OVARIAN CANCER
TITLE OF INVENTION: THERAPY OF OVARIAN CANCER
FILE REPRENCE: MRI-006B
CURRENT APPLICATION NUMBER: US 60/191,031
FRIOR APPLICATION NUMBER: US 60/191,031
FRIOR PILING DATE: 2000-03-21
FRIOR PELING DATE: 2000-06-15
FRIOR PELING DATE: 2000-06-15
FRIOR PELING DATE: 2000-06-15
FRIOR PELING DATE: 2000-07-07
FRIOR PELING DATE: 2000-07-07
FRIOR PELING DATE: 2000-07-25
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FRIOR PELING DATE: 2000-07-25
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549,
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Pred. No. 1.1;
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547,
609
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543, 544, 9
591, 595, 6
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LOCATION: 457, 458, 459, 461, 473,

LOCATION: 497, 512, 521, 527, 540,

LOCATION: 569, 584, 586, 587, 589,

COTHER INFORMATION: n = A,T,C or G
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Best Local Similarity 36.8%;
Matches 120; Conservative
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207 ACTACRIGITCTCTTCTAAGICCCACICCTCTTTTCTTTGAGCAGGAAAGAAAGAAAGCA 266
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CURRENT FILING DATE: 2002-06-13
NUMBER OF SEQ ID NOS: 116
SEQ ID NO 5
LENGTH: 9884
                                                                                                                                                                                                                                                                                                                                       327 AGGIGCAGCAGAGCCCTTTTCTTCCC 352
                                                                                                                                                                                                                                                                                                                                                                                                            334 CNCCCCCCNAANANNTTNCCCCCC 359
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Best Local Similarity 62.24
Matches 69, Conservative
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US-10-311-455-1449/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                147 AAGCAACGCTTGAAAAAAGGAAAGTTAGCCCTATCGGGTATATTTTGGAAGTTGTAAAAT 206
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Fublication No. US20030165831A1
Fublication No. US20030165831A1
Fublication No. US20030165831A1
Fublication No. US20030165831A1
Fublication No. US20030165831A1
Fublicant: Linile, James
Fublicant: Thompson, Pamela
APPLICANT: Thompson, Pamela
FAPPLICANT: Linile, James
ITTLE OF INVENTION: IDENTIFICATION, ASSESSMENT, PREVENTION, AND
FILLE OF INVENTION: IDENTIFICATION, ASSESSMENT, PREVENTION, AND
FILLE OF INVENTION: IDENTIFICATION, ASSESSMENT, PREVENTION, AND
FILLE OF INVENTION: IDENTIFICATION NUMBER: US 60/191,031
FRIOR FILING DATE: 2000-03-21
FRIOR FILING DATE: 2000-05-25
FRIOR FILING DATE: 2000-06-15
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LOCATION: 50, 99, 103, 104, 105, 106, 107, 108, 112, 114, 120, 121,
LOCATION: 122, 127, 128, 131, 132, 133, 134, 150, 151, 152, 153, 154,
LOCATION: 155, 156, 157, 158, 159, 160, 161, 162, 163, 183, 184, 186,
LOCATION: 188, 189, 190, 192, 193, 195, 196, 197, 209, 221, 223
OTHER INFORMATION: n = A,T,C or G
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NAME/KEY: misc_feature
LOCATION: 457, 458, 459, 461, 473, 474, 475, 476, 478, 480, 487, 494,
LOCATION: 497, 512, 521, 527, 540, 543, 544, 547, 549, 550, 554, 568,
LOCATION: 569, 584, 586, 587, 589, 591, 595, 609
OTHER INFORMATION: n = A,T,C or G
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334 CNCCCCCCNAANANTTINCCCCCC 359
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LOCATION: 224, 225, 238, 245, 248, 255,
LOCATION: 277, 278, 279, 280, 289, 292,
LOCATION: 343, 346, 348, 349, 350, 353,
LOCATION: 385, 398, 408, 422, 423, 440,
OTHER INFORMATION: n = A,T,C or G
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ORGANISM: Homo sapiens
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214 AAAAAANGININTTTCCCCCCCCCCTTTTTINAANCCCCCCNTINIANNAAAAAAANTTTT 273
                                                                                                                                                                                                                                 274 TINNNNNCCITITITGNGGNNAAAAAAAAAAAGGGGNTTITITITTTTGCNTTTTTCCNGGA 333
                                                                                                                      267 GTCACCCTCTCCATGACAACCCATGACCGGCTGCTTGCCTGCTCCATCACAGA
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Publication No. US20030113750A1
GENERAL INFORMATION:
APPLICANT: Epigenomics AG
TITLE OF INVENTION: Method and nucleic acids for the differentiation
TITLE OF INVENTION: of prostate tumors
FILE REFERENCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: DNA
ORGANISM: Artificial Sequence
FRATURE:
OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
US-10-172-086-5
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75 ITTATTCCCAAATTTTTCTTAAGCAAATATTTCTTTGCTAATCAATAAATTATCAAAAGA
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APPLICANT: Lillie, James
TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS ITILE OF INVENTION: IDENTIFICATION, ASSESSMENT, PREVENTION, AND TITLE OF INVENTION: THERAPY OF OVARIAN CANCER
FILE REFERENCE: MRI-006B
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                                                                                                                                TYPE: DNA
ORGANISM: BOS taurus
1 OTHER INFERMATION: Clone ID: 40-LIB3058-035-Q1-K1-B8
US-09-960-352-9335
                                                                                                                                                                                                                                     8.2%; Score 43.2; DB 10;
56.2%; Pred. No. 1.2;
tive 0; Mismatches 63;
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8.2%; Score 43.2; DB
Best Local Similarity 54.4%; Pred. No. 1.2;
Matches 87; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CURRENT APPLICATION NUMBER: US/09/814,353
CURRENT FILING DATE: 2001-03-21
PRIOR PILING DATE: 2001-03-21
PRIOR FILING DATE: 2000-03-21
PRIOR FILING DATE: 2000-03-21
PRIOR PLICATION NUMBER: US 60/191,031
PRIOR PLICATION NUMBER: US 60/21,940
PRIOR APPLICATION NUMBER: US 60/211,940
PRIOR PELING DATE: 2000-06-15
PRIOR PELING DATE: 2000-07-07
PRIOR PELING DATE: 2000-07-07
PRIOR PELING DATE: 2000-07-07
PRIOR APPLICATION NUMBER: US 60/226,661
PRIOR PELING DATE: 2000-07-25
PRIOR PELING DATE: 2000-12-21
PRIOR PELING DATE: 2000-12-21
FILE REFERENCE: 16511.006/37-21(10298)C
CURRENT APPLICATION NUMBER: US/09/960,352
CURRENT FILING DATE: 2001-09-24
NUMBER OF SEQ ID NOS: 15112
SEQ ID NO 9335
LENGTH: 380
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LENGTH: 397
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            147 AAGCAACGCTTGAAAAAAGGAAAG 170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      169 AAAAAAATTAAAAAAAAAAAA 192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 17565, Application US/09814353
Publication No. US20030165831A1
GENERAL INFORMATION:
APPLICANT: Lee, John
                                                                                                                                                                                                                                                                                 81; Conservative
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US-09-814-353-17565
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Best Local Similarity
Matches 81; Conserv;
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US-09-814-353-17565/c
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APPLICANT: Warren, Wengbing
APPLICANT: Tao, Nengbing
APPLICANT: Byatt, John C.
APPLICANT: Byatt, John C.
TITLE OF INVENTION: NUCLEIC ACID AND OTHER MOLECULES ASSOCIATED WITH LACTATION AND TITLE OF INVENTION: MUSCLE AND FAT DEPOSITION
FILE REPERENCE: 16511.006/37-21(10298)C
CURRENT APPLICATION NUMBER: US/09/960,352
CURRENT FILING DATE: 2001-09-24
NUMBER OF SEQ ID NOS: 15112
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Patent No. US20020137139A1

GENERAL INFORMATION:
APPLICANT: Warren, Wesley C.
APPLICANT: Byatt, John C.
APPLICANT: Byatt, John C.
APPLICANT: Byatt, John C.
APPLICANT: Byatt, John C.
APPLICANT: Byatt, John C.
APPLICANT: Mathialagan, NGGADPAND OTHER MOLECULES ASSOCIATED WITH LACTATION AND TITLE OF INVENTION: NUCLEIC AND FAI DEPOSITION
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                                                  Length 6590;
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Pred. No. 1.1;
1; Mismatches 112; Indels 0
                                                                                         Indels
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ORGANISM: Bos taurus
OTHER INFORMATION: Clone ID: 48-LIB3058-026-01-K1-D12
                                                  DB 13;
                                                                                       0; Mismatches
                                                  Score 43.6;
Pred. No. 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                              ; Sequence 11218, Application US/09960352; Patent No. US20020137139A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                    AAGCAACGCTTGAAAAA 164
                                                                                                                                                                                                                                                                                                                                            968 AATAAACACGTAAACAAA 951
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ilarity 57.2%;
Conservative
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Best Local Similarity 49.3°
Matches 110; Conservative
                                                                   Local Similarity
les 79; Conserv
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        JS-10-311-455-1449
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135 AAAAAAACTGAAAGCACGCTTGAAAAAAAGGAAGGTTG 174

Search completed: February 14, 2004, 14:16:16 Job time : 357 secs

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(a) assessing whether a patient is afflicted with prostate cancer;
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(a) assessing whether a patient is afflicted with prostate cancer;
(b) monitoring the progression of prostate cancer in a patient;
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         (d) assessing the efficacy of a therapy for inhibiting prostate cancer in a patient;
(e) selecting a composition for inhibiting prostate cancer in a patient;
(f) assessing the prostate cell carcinogenic potential of a compound;
(g) determining whether prostate cancer has metastasized in a patient;
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                                                                                                                                                                                                                                                                                                                                                                              82 CCAAATTTTTCTTAAGCAAATATTTCTTTGCTAATCAATAAATTATCAAAAGAAAAAAA 141
                                                                                                                                                                   81
                                                                                                                                                                                                                                  9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         human; prostate cancer; cytostatic; carcinogen; pharmacodyanamic marker;
pharmacogenomic marker; gene; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Novel isolated nucleic acid molecule associated with cancerous state of prostate cells and correlating with presence of prostate cancer, useful for detecting presence of prostate cancer -
                                                                                                                                                                                                                                         Gaps
                                                                                            ö
              Score 50.4; DB 23; Length 556;
Pred. No. 0.02;
                                                                                        61; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human prostate expression marker cDNA 43592.
                                                                                            0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 1; Page 8681-8682; 11750pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                         142 ACTGAAAGCAACGCTTGAAAAAAGGAAA 169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           121 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 148
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                  9.5%;
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2000US-211314P.
2000US-219007P.
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16-MAR-2000; 2000US-189862P.
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13-DEC-2000; 2000US-255281P
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Query Match
Best Local Similarity 58.8'
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from cattle, and the LMFD nucleic acid can specifically hybridise to a second nucleic acid can specifically hybridise to a second nucleic acid molecule comprising any of 15112 nucleotide
second nucleic acid molecule comprising any of 15112 nucleotide
comprising an LMFD nucleic acid linked to a promoter and a 3' non-
translated sequence that functions in the cell to cause termination of transcription and addition of polyadenylated ribonucleotides to a 3' end
comprising an LMFD nucleic acid linked to a promoter and a 3' non-
transcription and addition of polyadenylated ribonucleotides to a 3' end
complement and addition of polyadenylated ribonucleotides to a 3' end
complement or fragment) with a complementary nucleic acid sequences or its
complement or fragment) with a complementary nucleic acid molecule
complementary nucleic acid and the complementary nucleic acid permits the
detection of the molecule; and (b) detecting the level or pattern of the
complementary nucleic acid, where the detection of the molecule.
The LMFD nucleic acid is used for determining a level or pattern
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   26 ATTTATATGCTGATTTATGGGTGATTTTGCTTCCTTCTTTATACTTTTATTTCCCAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /product= involved in extrachromosomal replication
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Note: The present sequence was not shown in the specification but was obtained in electronic format from the USPTO web site:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   9.4%; Score 49.6; DB 25; Length 424; 59.0%; Pred. No. 0.028; 1ive 0; Mismatches 59; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       seqdata.uspto.gov/sequence.html?DocID=20020137139.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Seguence 424 BP; 228 A; 7 C; 32 G; 157 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Dictyostelium plasmid Ddp2 containing Rep gene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    slime mould; replication; Rep gene; ss
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAAGCAACGCTTGAAAAAAGGAAA 169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAAAAAAAACCAAAAAAAAAA 49
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2378..5041
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(first entry)
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nes 85; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    selecting a composition for inhibiting prostate cancer in a patient, assessing the prostate cell carcinogenic potential of a compound; determining whether prostate cancer has metastasized in a patient; assessing the aggressiveness or indolence of prostate cancer in a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (a) assessing whether a patient is afflicted with prostate cancer; (b) monitoring the progression of prostate cancer in a patient; (c) assessing the efficacy of a test compound to inhibit prostate cancer in a patient; (d) assessing the efficacy of a therapy for inhibiting prostate cancer in a patient; (e) selecting a composition for inhibiting prostate cancer in a sessessing the prostate cell carcinogenic potential of a compound; (f) assessing the prostate cell carcinogenic potential of a compound; (g) determining whether prostate cancer has metastasized in a patient; (h) assessing the aggressiveness or indolence of prostate cancer in a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bovine, 88; EST; expressed sequence tag; lactation; LMFD; muscle deposition; fat deposition; genome mapping; gene identification; gene analysis; cattle breeding.

    is also useful as a pharmacodyanamic or pharmacogenomic marker.

                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bovine EST associated with lactation/muscle/fat deposition #11218.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               deposition, useful for genome mapping, gene identification and analysis, cattle breeding, or for genetically improving cattle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New nucleic acid associated with lactation, and muscle and fat
                                                                                                                                                                                                                                                                                                                                                                                                                                9.5%; Score 50.4; DB 23; Length 556; 58.8%; Pred. No. 0.02; Live 0; Mismatches 61; Indels 0.
                                                                                                                                                                                                                                                                                                                                                                           Sequence 556 BP; 389 A; 1 C; 51 G; 113 T; 2 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ACTGAAAGCAACGCTTGAAAAAAGGAAA 169
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11-JAN-2000; 2000US-0480902.
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les 87; Conservative
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MATHIALAGAN N.
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                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
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90WO-AU00530. 89AU-0007187.

02-NOV-1990; 02-NOV-1989;

The invention relates to a purified nucleic acid molecule associated with

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Monahan JE

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Schlegel R, Endege WO,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAH71471;
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                                                                                                                                                                                                                                                               Query Match
                                                                                                                                                                                                                                                                         Local
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                                                                                                                                                                                                                                                                                                    5708
                                                                                                                                                                                                                                                                                                                                        TRATITATICCCAAATTTTTCTTAAGCAAATATTTCTTTGCTAATCAATAAATTATCAAA 131
                                                                                                                                                                                                                                                                                  71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human; prostate cancer; cytostatic; carcinogen; pharmacodyanamic marker; pharmacogenomic marker; gene; 88.
                                                                                                                                                                                                                                                                                                    The sequence of Ddp2 has been found to contain the putative open reading frame indicated in the Features Table. The possible ORF is flanked by regions with similarity to promoter and poly adenylation signals of known Dictyostellum genes. The RNA and polypeptide product of the Reg gene have note, however, been detected. It is believed that the product is produced in low amounts to positively regulate initiation of plasmid replication. The polypeptide may also contain regions that act as negative regulators of plasmid copy (Updated on 25-WAR-2003 to correct PA field.)
                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                            Score 49.2; DB 12; Length 5852;
Pred. No. 0.076;
0; Mismatches 68; Indels 0;
                                                                         ъ
•
                                                                                                                                                                                                                          Sequence 5852 BP; 2298 A; 651 C; 708 G; 2195 T; 0 other;
                                                                        Polypeptide facilitating extra-chromosomal replication recombinant plasmid in Dictyostelium species
                                                                                                                                                                                                                                                                                                                                                                            5647 AAAAAAAAATTTAAATTAAAAAAAAAAAAAAAA 5610
                                                                                                                                                                                                                                                                                                                                                            AGAAAAAAAACTGAAAGCAACGCTTGAAAAAAGGAAA 169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human prostate expression marker cDNA 3801.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
                          Williams KL;
                                                                                                   Claim 15, Fig 1, 90pp; English.
                                                                                                                                                                                                                                            Query Match

9.3%;

Best Local Similarity 57.0%;

Matches 90; Conservative (
                                                                                                                                                                                                                                                                                                                                                                                                                           ABV03810 standard; cDNA; 464
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2000US-189862P.
2000US-207454P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2000US-211314P
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2000US-255281P
                                                                                                                                                                                                                                                                                                                                                                                                                                                               13-SEP-2002 (first entry)
        (UYMA-) UNIV MACQUARIE
                          Chang ACM,
                                            WPI; 1991-164194/22.
P-PSDB; AAR11988.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WO200160860-A2
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25-MAY-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       13-DEC-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     23-AUG-2001
                          Slade MB,
                                                                                                                                                                                                                                                                                                                                                           132
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                                                                                                                                                                                                                                                                                                                                                                                                                                             ABV03810;
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The invention relates to an isolated nucleic acid molecule (I) comprising a nucleotide sequence given in Tables 1-9 (ABV00010-ABV62213) of the specification or its complement. (I) is useful for:

(a) assessing whether a patient is afflicted with prostate cancer;

(b) monitoring the progression of prostate cancer in a patient;

(c) assessing the efficacy of a test compound to inhibit prostate cancer.

(d) assessing the efficacy of a therapy for inhibiting prostate cancer.

(d) assessing the efficacy of a therapy for inhibiting prostate cancer.

(e) selecting a composition for inhibiting prostate cancer in a patient;

(f) assessing the prostate cell carcinogenic potential of a compound;

(f) assessing the aggressiveness or indolence of prostate cancer in a patient;

(h) assessing the aggressiveness or indolence of prostate in a patient;
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of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    248 AACCCCCINCCAAININNAAAAINIAAAAACCCCIAINININGACINGTAAAAAAAAAA 307
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   67
Novel isolated nucleic acid molecule associated with cancerous state of prostate cells and correlating with presence of prostate cancer, useful for detecting presence of prostate cancer -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Cervical cancer; cytostatic; pre-malignant condition; gene therapy; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     147 AAGCAACGCTTGAAAAAAGGAAAGTTAGCCCTATCGGGTATATTTTGGAAGTTGTAAAAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                207 ACTACRIGITCTCTTCTAAGTCCCACTCCTCTTTTTTTTTGAGCAGGAAAGAGAAAGCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GTCACCCTCTCTTCCATGACAACAACCCATGACGGCTGCTTGCCTGCTCCATCACAGGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TITATATGCTGATTTATGGGTGATTTTGCTTCCTTCTTTATACTTTTATTTTCCCAAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (I) is also useful as a pharmacodyanamic or pharmacogenomic marker
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           9.2%; Score 48.6; DB 23; Length 464; 43.3%; Pred. No. 0.05;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 464 BP; 199 A; 74 C; 16 G; 116 T; 59 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1; Mismatches 172;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human cervical cancer marker nucleic acid 2745,
                                                                                                                                  Claim 1; Page 677; 11750pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    멾.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches 132; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AGGTG 331
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selecting a composition for inhibiting prostate cancer in a patient; assessing the prostate cell carcinogenic potential of a compound; determining whether prostate cancer has metastasized in a patient; assessing the aggressiveness or indolence of prostate cancer in a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      cancer; cytostatic; carcinogen; pharmacodyanamic marker; marker; gene; 88.
                                                                                                                                                                                                                  Novel isolated nucleic acid molecule associated with cancerous state of prostate cells and correlating with presence of prostate cancer, useful for detecting presence of prostate cancer -
                                                                                                                                                                                                                                                                                                                                                                                                                                                        cancer in a patient; (d) assessing the efficacy of a therapy for inhibiting prostate cancer in a patient;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        34 GCTGATTTATGGGTGATTTTGCTTCCTTCTTTATACTTTTATTTTATTCCCAAATTTTTCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The invention relates to an isolated nucleic acid molecule (I) compared in mucleotide sequence given in Tables 1-9 (ABV00010-ABV62213) of the specification or its complement. (I) is useful for:
(a) assessing whether a patient is afflicted with prostate cancer;
(b) monitoring the progression of prostate cancer in a patient;
(c) assessing the efficacy of a test compound to inhibit prostate

    is also useful as a pharmacodyanamic or pharmacogenomic marker.

                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ch 9.1%; Score 48; DB 23; Length 474; I Similarity 59.6%; Pred. No. 0.07; 81; Conservative 0; Mismatches 55; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 474 BP; 234 A; 34 C; 107 G; 98 T; 1 other;
                                                                                                 (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
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                                                                                                                                                                                                                                                                                                 Claim 1; Page 10898; 11750pp; English
                                                                                                                                          Monahan JE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 154 GCTTGAAAAAAGGAAA 169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        129 AAAAAAAAAAAAAA 144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ABV04310 standard; cDNA; 300
25-MAY-2000; 2000US-207454P.
09-JUN-2000; 2000US-211314P.
18-JUL-2000; 2000US-219007P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        20-FEB-2001; 2001WO-US05171.
                                                           13-DEC-2000; 2000US-255281P
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                                                                                                                                          Endege WO,
                                                                                                                                                                               WPI; 2001-662795/76.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Local Similarity
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pharmacogenomic
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                                                                                                                                          Schlegel R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 13-SEP-2002
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        cervical cancer with cytostatics are actively. The nucleic acids and encoded polypeptides are useful: to assess if a patient is afflicted with cervical cancer or has a pre-malignant condition; to monitor the progression of cervical cancer or a premalignant condition in a patient, and to select and/or assess the efficacy of a compound or therapy for inhibiting cervical cancer in a patient. The nucleic acids may also be useful for gene therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TITATATGCTGATTTATGGGTGATTTTGCTTCCTTTTATACTTTTATTTCCCAAA 86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      16
                                                                                                                                                                                                                                                                                                                                                                                                                                    The invention relates to novel genes (AAH68727-AAH73383) associated with
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human; prostate cancer; cytostatic; carcinogen; pharmacodyanamic marker; pharmacogenomic marker; gene; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                    isolated nucleic acid for diagnosing and treating cervical car for assessing and detecting compounds for treating the cancer
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0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 612 BP; 380 A; 50 C; 2 G; 178 T; 2 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 48.6; DB 22;
Pred. No. 0.054;
0; Mismatches 59;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human prostate expression marker cDNA 56483.
                                                                                                                                                                                                                    (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
                                                                                                                                                                                                                                                          Berger A, Zhao X;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               137 AAAAAAAAATAAAAAAAAAAAA 159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        147 AAGCAACGCTTGAAAAAAGGAAA 169
                                                                                                                                                                                                                                                                                                                                                                                               Claim 1; Page 564; 1051pp; English
                                                                             99US-0169681.
99US-0171350.
2000US-0189315.
2000US-0203791.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ch 9.2%;
1 Similarity 58.7%;
84; Conservative (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ABV56492 standard; cDNA; 474
                                        2000WO-US33312
                                                                                                                                                                             21-JUL-2000; 2000US-0220114
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16-MAR-2000; 2000US-189862P
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                                                                                                                                                                                                                                                          Schlegel R, Deeds J,
                                                                                                                                                                                                                                                                                               WPI; 2001-375006/39
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                                        08-DEC-2000;
                                                                                                                    14-MAR-2000;
                                                                                                                                        12-MAY-2000;
                                                                               08-DEC-1999;
                                                                                                   21-DEC-1999;
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  14-JUN-2001
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Best Local S
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us-10-027-632-1.rng

Homo sapiens.

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(a) assessing whether a patient is afflicted with prostate cancer;
(b) monitoring the progression of prostate cancer in a patient;
(c) assessing the efficacy of a test compound to inhibit prostate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TGAAAAATTINNTTTTTTTGGAATTTTTTTTTTTTTTTTCCCTTTTAAATTTTTTT 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     selecting a composition for inhibiting prostate cancer in a patient, assessing the prostate cell carcinogenic potential of a compound; determining whether prostate cancer has merastasized in a patient; assessing the aggressiveness or indolence of prostate cancer in a
                                                                                                                                                                                                                                Novel isolated nucleic acid molecule associated with cancerous state of prostate cells and correlating with presence of prostate cancer, useful for detecting presence of prostate cancer -
                                                                                                                                                                                                                                                                                                                                                                                                                                                   cancer in a patient; (d) assessing the efficacy of a therapy for inhibiting prostate cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TGATTTATATGCTGATTTATGGGTGATTTTGCTTCCTTCTTTATACTTTTATTTCCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gape

    is also useful as a pharmacodyanamic or pharmacogenomic marker.

                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             antiarteriosclerotic; antianaemic; cytostatic; nootropic;
neuroprotective; anti-HIV; anticonvulsant; ophthalmological;
antirheumatic; antiarthritic; antidiabetic; antipsoriatic;
antiinflammatory; cancer; eye disease; arteriosclerosis; anaemia;
acute myeloid leukaemia; Alzheimer's disease; AIDS; epilepsy;
neurofibromatosis; rheumatoid arthritis; psoriasis; bowel disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human; immune system disease; cytosine methylation; antiasthmatic;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Match 9.0%; Score 47.8; DB 23; Length 300; Local Similarity 56.2%; Pred. No. 0.068; es 82; Conservative 0; Mismatches 64; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 300 BP; 125 A; 22 C; 19 G; 101 T; 33 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human immune system associated gene SEQ ID NO: 2148
                                                                                                                         (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      144 TGAAAGCAACGCTTGAAAAAAGGAAA 169
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                                                                                                                                                              Monahan JE;
                                                                                                                                                                                                                                                                                                       Claim 1; Page 750; 11750pp; English
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                  ; 2000US-189862P.
; 2000US-207454P.
; 2000US-211314P.
; 2000US-219007P.
 2000US-183319P
                                                                                      13-DEC-2000; 2000US-255281P
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                                                                                                                                                              Endege WO,
                                                                                                                                                                                              WPI; 2001-662795/76.
                                                  09-JUN-2000;
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                  16-MAR-2000;
25-MAY-2000;
 17-FEB-2000;
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                                                                                                                                                         Schlegel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ABL34175;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          gene; da.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
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Matches
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ABL34175/
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41662 CTTCTTTGTTTATACAATTAATAATTACTTTCTATTTTAAAACAAAACTTTATCTTTTT 41603
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                                                                                                                                                                                                                                                                                                                                                                                 The present invention provides a number of human immune system associated genes which are modified by the methylation of cytosines. The sequences can be used in the diagnosis and treatment of immune system disorders, including eye diseases such as retinopathy, neovascular glaucome and macular degeneration, arteriosclerosis, anaemia, cancer, acute myeloid leukaemia, Alzhaimer's disease, AIDS, epilepsy, neurofibromatosis, rheumatoid arthritis, psoriasis and inflammatory/ulcerative bowel diseases. The present sequence is a gene of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   115 ATCAATAAATTATCAAAAGAAAAAAAACTGAAAGCAACGCTTGAAAAAAGGAAAGTTAG 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human; prostate cancer; cytostatic; carcinogen; pharmacodyanamic marker; pharmacogenomic marker; gene; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              55 CTTCCTTCTTTATACTTTTATTCCCAAATTTTTCTTAAGCAAATATTTCTTTGCTA
                                                                                                                                                                                                                                                                                  Nucleic acid comprising fragment of chemically modified gene, useful for diagnosis and treatment of diseases associated with abnormal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    41542 Troccaccarratrratrratratratrcaarriraacrrataa 41492
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 47.4; DB 24; Length 113515;
Pred. No. 0.49;
1; Mismatches 77; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      175 CCCTATCGGGTATATTTTGGAAGTTGTAAAATACTACRTGTTCTCTTCTAA 225
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 113515 BP; 35172 A; 1174 C; 22520 G; 54649 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                        Claim 1; SEQ ID NO 2148; 32pp + Sequence Listing; German
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human prostate expression marker cDNA 44985
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                                                                                                                                                                                                                    Berlin
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  20-FEB-2001; 2001WO-US05171.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  17-FEB-2000; 2000US-183319P.
                                                                                                                               30-JUN-2000; 2000DE-1032529
01-SEP-2000; 2000DE-1043826
                                                                                                 02-JUL-2001; 2001WO-EP07537
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              93; Conservative
                                                                                                                                                                                                                    Olek A, Piepenbrock C,
                                                                                                                                                                                (BPIG-) EPIGENOMICS AG
                                                                                                                                                                                                                                                                                                                        cytosine methylation
                                                                                                                                                                                                                                                    WPI; 2002-130909/17.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Similarity
                               WO200200928-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens
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                                                                 03-JAN-2002
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Best Local
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selecting a composition for inhibiting prostate cancer in a patient; assessing the prostate cell carcinogenic potential of a compound; determining whether prostate cancer has metastasized in a patient; assessing the aggressiveness or indolence of prostate cancer in a
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                                                                                                                                                                                                                                                                                                                                                                                                                      Novel isolated nucleic acid molecule associated with cancerous state of prostate cells and correlating with presence of prostate cancer, useful for detecting presence of prostate cancer -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The invention relates to an isolated nucleic acid molecule (I) comprisis a nucleotide sequence given in Tables 1-9 (ABV00010-ABV62213) of the specification or its complement. (I) is useful for:
(a) assessing whether a patient is afflicted with prostate cancer;
(b) monitoring the progression of prostate cancer in a patient;
(c) assessing the efficacy of a test compound to inhibit prostate cancer in a patient;
(d) assessing the efficacy of a therapy for inhibiting prostate cancer.

    is also useful as a pharmacodyanamic or pharmacogenomic marker.

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 47; DB 23
Pred. No. 0.11;
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                                                                                                                                                                                                                                          (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 1; Page 8916; 11750pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    147 AAGCAACGCTTGAAAAAAGGAAA 169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            87 AAAAAAAAAAAAAAAAAAA 65
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                            17-FEB-2000; 2000US-183319P.
16-MAR-2000; 2000US-189862P.
25-MAY-2000; 2000US-207454P.
9-UJN-2000; 2000US-211314P.
18-UJL-2000; 2000US-21914P.
13-DEC-2000; 2000US-255281P.
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                                                                                                                                                                                                                                                                                                      Endege WO,
                                                                                                                                                                                                                                                                                                                                                              WPI; 2001-662795/76.
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(a) assessing whether a patient is afflicted with prostate cancer;
(b) monitoring the progression of prostate cancer in a patient;
(c) assessing the efficacy of a test compound to inhibit prostate cancer in a patient;
(d) assessing the efficacy of a therapy for inhibiting prostate cancer in a patient;
(e) selecting a composition for inhibiting prostate cancer in a patient;
(f) assessing the prostate call carcinogenic potential of a compound;
(g) determining whether prostate cancer has metastasized in a patient;
(h) assessing the aggressiveness or indolence of prostate cancer in a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human; prostate cancer, cytostatic; carcinogen; pharmacodyanamic marker; pharmacogenomic marker; gene; ss.
                                                                                                                                                                                                                                                                                                                                                           Novel isolated nucleic acid molecule associated with cancerous state of prostate cells and correlating with presence of prostate cancer, useful for detecting presence of prostate cancer -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 27 TTTATATGCTGATTTATGGGTGATTTTGCTTCCTTCTTTATACTTTTATTATTCCCAAA

    is also useful as a pharmacodyanamic or pharmacogenomic marker.

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Seguence 309 BP; 188 A; 13 C; 11 G; 97 T; 0 other;
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                                                                                                                                                                               (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 1; Page 8916; 11750pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 153 AAAAAAAAAAAAAAAAAAAA 175
                                                                                                                                                                                                                                       Schlegel R, Endege WO, Monahan JE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ABV44994 standard; cDNA; 309
                            25-MAY-2000; 2000US-207454P.
09-JUN-2000; 2000US-211314P.
18-JUL-2000; 2000US-219007P.
2000US-189862P.
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                                                                                                                   13-DEC-2000; 2000US-255281P
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Local Similarity
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XX AC ABV44991
XX ID 16-SEP-
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XX Human 1
XX Human 5
XX Homo 63
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The invention relates to novel genes (AAH68727-AAH73383) associated with cervical cancer with cytostatic activity. The nucleic acids and encoded polypeptides are useful: to assess if a patient is afflicted with cervical cancer or has a pre-malignant condition; to monitor the progression of cervical cancer or a premalignant condition in a patient; and to select and/or assess the efficacy of a compound or therapy for inhibiting cervical cancer in a patient. The nucleic acids may also be useful for gene therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bovine; 88; EST; expressed sequence tag; lactation; LMFD; muscle deposition; fat deposition; genome mapping; gene identification; gene analysis; cattle breeding.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  isolated nucleic acid for diagnosing and treating cervical cancer for assessing and detecting compounds for treating the cancer -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TITATATGCTGATTTATGGGTGATTTTGCTTCCTTTTATATTTTATTTCCCAAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 8.9%; Score 47; DB 22; Length 612; Best Local Similarity 58.0%; Pred. No. 0.13; Matches 83; Conservative 0; Mismatches 60; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 612 BP; 380 A; 50 C; 2 G; 178 T; 2 other;
                                                                                                                                                                                                        (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA
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                                                                                          99US-0171350.
                                   08-DEC-2000; 2000WO-US33312
                                                                                                                              2000US-0203791
2000US-0210600
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                                                                                        21-DEC-1999;
14-MAR-2000;
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                                                                        08-DEC-1999;
14-JUN-2001
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                                                                                                                                                                                                                                                                                                                                                                                                         The invention relates to an isolated nucleic acid molecule (I) comprising a nucleotide sequence given in Tables 1-9 (ABV00010-ABV62213) of the specification or its complement. (I) is useful for:
(a) assessing whether a patient is afflicted with prostate cancer;
(b) monitoring the progression of prostate cancer in a patient;
(c) assessing the efficacy of a test compound to inhibit prostate cancer in a patient;
(d) assessing the efficacy of a therapy for inhibiting prostate cancer in a patient;
(e) selecting a composition for inhibiting prostate cancer in a patient;
(f) assessing the prostate call carcinogenic potential of a compound;
(g) determining whether prostate cancer has metastaaized in a patient;
(h) assessing the aggressiveness or indolence of prostate cancer in a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    146
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                                                                                                                                                                                                                                                                                                 Novel isolated nucleic acid molecule associated with cancerous state of prostate cells and correlating with presence of prostate cancer, useful for detecting presence of prostate cancer -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Cervical cancer; cytostatic; pre-malignant condition; gene therapy; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (I) is also useful as a pharmacodyanamic or pharmacogenomic marker
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 23; Length 474;
0.12;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human cervical cancer marker nucleic acid 2745
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 47; DB 2; Pred. No. 0.12; 0; Mismatches
                                                                                                                                                                                     (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
                                                                                                                                                                                                                                                                                                                                                                            Claim 1; Page 10898; 11750pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           147 AAGCAACGCTTGAAAAAAGGAAA 169
                                                                                                                                                                                                                          Monahan JE
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                 20-PEB-2001; 2001WO-US05171.
                                                                                        2000US-207454P.
                                                     2000US-183319P
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                                                                                                                                                                                                                                                              WPI; 2001-662795/76.
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                                                                                        25-MAY-2000;
                                                     17-FEB-2000;
                                                                        16-MAR-2000;
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99US-115707P

12-JAN-1999;

WO200142467-A2 Ното варіепв

24-SEP-2001; 2001US-0960352

26-SEP-2002

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The invention relates to a purified nucleic acid molecule associated with lactation or muscle and fat deposition (designated LWED), derived from cattle, and the LMFD nucleic acid can specifically hybridise to a second nucleic acid molecule comprising any of 15112 nucleotide comprising an LMED nucleic acid linked to a promoter and a 3' non-comprising an LMED nucleic acid linked to a promoter and a 3' non-comprising an LMED nucleic acid linked to a promoter and a 3' non-comprising an LMED nucleic acid linked to a promoter and a 3' non-comprising an LMED nucleic acid linked to a promoter and a 3' non-comprising an addition of polyadenylated ribonucleotides to a 3' end complement cell or tissue comprising; (a) incubating a marker nucleic acid (comprising any of the 15112 nucleic acid sequences or its complement or fragment) with a complementary nucleic acid and the complementary nucleic acid and the complementary nucleic acid and the complementary nucleic acid and the complementary nucleic acid acid where the detection of the molecule.

Complementary nucleic acid, where the detection of the molecule.

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Complementary nucleic acid, where the detection of the molecule.

Complementary nucleic acid is used for determining a level or pattern of the LMED nucleic acid is predictive of the level or pattern of the molecule in a bovine cell or tissue. It is useful for genome mapping sene identification and analysis, cattle breeding, preparation of constructs for use in cattle genese expression, or for genome mapping contents for use in cattle genese considered is one of the 15112 bovine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     t shown in the specification but from the USPTO web site:
                                                                                                                                                                                    New nucleic acid associated with lactation, and muscle and fat deposition, useful for genome mapping, gene identification and analysis, cattle breeding, or for genetically improving cattle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 312 BP; 167 A; 27 C; 28 G; 90 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       segdata.uspto.gov/sequence.html?DocID=20020137139.
                                                                                                                     Tao N, Warren WC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       e: The present sequence was not shown
obtained in electronic format from the
                                                                                                                                                                                                                                                          Claim 2; SEQ ID No 8414; 245pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (expressed sequence tag)
11-JAN-2000; 2000US-0480902
                                                                                                                   Mathialagan N,
                               BYATT J C.
MATHIALAGAN N.
                                                                                                                                                    WPI; 2003-110599/10
                                                                                 (WARR/) WARREN W C.
                                                                   TAO N.
                                                                                                                   Byatt JC,
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                                 (BYAT/)
                                                 (MATH/
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80 Gaps .; 0 ch 8.8%; Score 46.6; DB 25; Length 312; 1 Similarity 57.0%; Pred. No. 0.13; 85; Conservative 0; Mismatches 64; Indels 0 141 AACTGAAAGCAACGCTTGAAAAAAGGAAA 169 Query Match Best Local Similarity Matches 8 셤 ઠે g ò

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Human leukocyte derived cDNA SEQ ID NO 8192.
    145 ААААААААААСААААААААААААААА 173
                                                                     ABZ08201 standard; cDNA; 480
                                                                                                                           09-JAN-2003 (first entry)
                                                                                                ABZ08201;
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ID ABZ0
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AC ABZ0
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muscle deposition; fat deposition gene analysis; cattle breeding.

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The invention relates to a system for detecting gene expression, which comprises one or two isolated DNA molecules that detect expression of a gene, where the gene corresponds to any of 8143 oligomouslectides (ABZ00010-ABZ08152) each having 50 base pairs (bp). The system is useful for leukocyte expression profiling. It is particularly useful for diagnosing a disease, monitoring (rate of) progression of a disease, predicting therapeutic outcome, determining prognosis for a patient, predicting disease complications in an individual or monitoring response to treatment in an individual. The diseases include cardiac allograft rejection, kidney allograft rejection, liver allograft rejection, atherosclerosis, congestive heart failure, systemic lupus erythematosus, rheumatoid arthritis, osteoarthritis or cytomegalovirus infection. The present sequence is that of a human leukocyte expressed CDNA of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               142 ITTITACITITITITITICATATITITAATIACCAAAATAAAATAAAATAAAATAAAATTAA
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                          atherosclerosis; congestive heart failure; systemic lupus erythematosus; rheumatoid arthritis; osteoarthritis; cytomegalovirus; infection; gene;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New system for leukocyte expression profiling, diagnosing a disease, or monitoring (the rate of) progression of a disease, e.g. atherosclerosis or congestive heart failure, comprises diagnostic oligonucleotides -
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Gaps
Human; leukocyte; gene expression profiling; allograft rejection;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Altman.P, Prentice J, Johnson F;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 26; Page 1829-1830; 2038pp; English.
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                                                                                                                                                                                                                                                                                                                                              22-OCT-2001; 2001WO-US47856.
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08-JUN-2001; 2001US-296764P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (BIOC-) BIOCARDIA INC.
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Woodward R, Qu
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                                                                                                                                                                                                                   WO200257414-A2
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                                                                                                                                                        Homo sapiens
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ABV40063 standard; cDNA; 556 BP.
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                                                                                                                                                                                                                                                                                                                                                                                                                     The invention relates to a purified nucleic acid molecule associated with lactation or muscle and fat deposition (designated LMPD), derived from cattle, and the LMPD nucleic acid can specifically hybridise to a second nucleic acid molecule comprising any of 15112 nucleotide sequences, appearing as ABX34836-ABX49947, or complements of them. Also infoluded are; (1) a transformed cell having a nucleic acid comprising any of them. Comprising an LMPD nucleic acid linked to a promoter and a 3' nontranslated sequence that functions in the cell to cause termination of transcription and addition of polyadenylated ribonucleotides to a 3' end of the mRNA molecule; and (2) determining a level or pattern of a molecule in a bovine cell or tissue comprising: (a) incubating a marker nucleic acid (comprising any of the 15112 nucleic acid sequences or its complement or fragment) with a complementary nucleic acid molecule complementary nucleic acid permits the detection of the molecule; and (b) detecting the level or pattern of the complementary nucleic acid acid (sequence) and (b) detecting the level or pattern of the complementary nucleic acid is used the complementary nucleic acid sequence of the level or pattern of the molecule in a bovine cell or tissue. It is useful for genome of a molecule in a bovine cell or tissue. It is useful for genome of constructs for use in cattle gene expression, or for genetically improving cattle. The present sequence is an of the sequence is an of the constructs for use in cattle gene expression, or for genetically the constructs for the present sequence is an of the factor of the interval of the constructs for use in cattle gene expression, or for genetically the constructs for the molecule acid in a provine cell or the molecule acid in a provine cell or the molecule acid in the present sequence is an order or an order cell or the molecule or approve the molecule acid is used not cell or the molecule acid the molecule acid in acid is used not cell or the molecule acid the molecule acid the mol
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                                                                                                                                                                                                                                                                                                                              New nucleic acid associated with lactation, and muscle and fat deposition, useful for genome mapping, gene identification and
                                                                                                                                                                                                                                                                                                                                                deposition, useful for genome mapping, gene identification and analysis, cattle breeding, or for genetically improving cattle
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                                                                                                                                                                                                                                                                      Warren WC;
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57.1%; Pred. No. 0.16;
iive 0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                              Claim 2; SEQ ID No 8414; 245pp; English.
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                                                                                                          24-SEP-2001; 2001US-0960352.
                                                                                                                                        12-JAN-1999; 99US-115707P.
                                                                                                                                                                                                                                                                   Byatt JC, Mathialagan N,
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nes 84; Conservative
                                                                                                                                                                                      BYATT J C.
MATHIALAGAN N.
                                                                                                                                                                                                                                                                                                  WPI; 2003-110599/10.
                                                                                                                                                                                                   (MATH/) MATHIALAGAN
(TAON/) TAO N.
(WARR/) WARREN W C.
                                             US2002137139-A1
                                                                             26-SEP-2002
              Bos Taurus.
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                                                                                                                Human, prostate cancer; cytostatic, carcinogen, pharmacodyanamic marker; pharmacogenomic marker; gene; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          selecting a composition for inhibiting prostate cancer in a patient; assessing the prostate cell carcinogenic potential of a compound; determining whether prostate cancer has metastasized in a patient; assessing the aggressiveness or indolence of prostate cancer in a
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a assessing whether a parlient is afflicted with prostate cancer;
(b) monitoring the progression of prostate cancer in a patient;
(c) assessing the efficacy of a test compound to inhibit prostate cancer in a patient;
(d) assessing the efficacy of a therapy for inhibiting prostate cancer in a patient;
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    is also useful as a pharmacodyanamic or pharmacogenomic marker.

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                                                           Human prostate expression marker cDNA 40054.
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Pred. No. 0.3;
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25-MAY-2000; 2000US-207449P.
09-UUN-2000; 2000US-211314P.
18-JUL-2000; 2000US-219007P.
13-DEC-2000; 2000US-255281P.
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(first entry)
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16-SEP-2002
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147 AAGCAACGCTTGAAAAAGGAAA 169
                                                                              ABV42105 standard; cDNA; 556
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2000US-207454P.
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in a patient;
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                                                                                                   ABV42105;
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(a) assessing whether a patient is afflicted with prostate cancer;
(b) monitoring the progression of prostate cancer in a patient;
(c) assessing the efficacy of a test compound to inhibit prostate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                selecting a composition for inhibiting prostate cancer in a patient; assessing the prostate cell carcinogenic potential of a compound; determining whether prostate cancer has metastasized in a patient;
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                                                                                                                                            Human; prostate cancer; cytostatic; carcinogen; pharmacodyanamic marker; pharmacogenomic marker; gene; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                  Novel isolated nucleic acid molecule associated with cancerous state of prostate cells and correlating with presence of prostate cancer, useful for detecting presence of prostate cancer -
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                                                                                                                        Human prostate expression marker cDNA 40154
                                                                                                                                                                                                                                                                                                                                                 (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
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Pred. No. 0.3;
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                                                                                                                                                                                                                                                                                                                                                                         Monahan JE;
56 AAAAAAAAAAAAAAAAAAAAA 34
                                                      ABV40163 standard; cDNA; 556
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25-MAY-2000; 2000US-207454P.
09-JUN-2000; 2000US-211314P.
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nes 82; Conservative
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                                                                           ABV40163
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Novel isolated nucleic acid molecule associated with cancerous state of prostate cells and correlating with presence of prostate cancer, useful for detecting presence of prostate cancer -
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(a) assessing whether a patient is afflicted with prostate cancer;

(b) monitoring the progression of prostate cancer in a patient;

(c) assessing the efficacy of a test compound to inhibit prostate cancer in a patient;
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Pred. No. 0.3;
0; Mismatches 61; Indels 0
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56 AAAAAAAAAAAAAAAAAAAA 34
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The invention relates to an isolated nucleic acid molecule (I) comprising a nucleotide sequence given in Tables 1-9 (ABV00010-ABV62213) of the specification or its complement. (I) is useful for:
(a) assessing whether a patient is affilicted with prostate cancer;
(b) monitoring the progression of prostate cancer in a patient;
(c) assessing the efficacy of a test compound to inhibit prostate cancer in a patient;
(d) assessing the efficacy of a therapy for inhibiting prostate cancer in a patient;
(e) selecting a composition for inhibiting prostate cancer in a patient;
(f) assessing the prostate cell carcinogenic potential of a compound;
(g) determining whether prostate cancer has metastasized in a patient;
(h) assessing the aggressiveness or indolence of prostate cancer in a
 57
                                                                                                                                                                                                                                                                                                                     cancer; cytostatic; carcinogen; pharmacodyanamic marker;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       39 TITATGGGTGATITITGCTICCTICTITATACTITITATITCCCAAATTTTTCTTAAGC 98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Novel isolated nucleic acid molecule associated with cancerous state of prostate cells and correlating with presence of prostate cancer, useful for detecting presence of prostate cancer -
                 Gapa

    is also useful as a pharmacodyanamic or pharmacogenomic marker.

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 464 BP; 199 A; 74 C; 16 G; 116 T; 59 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
                                                                                                                                                                                                                                                                                    Human prostate expression marker cDNA 3801
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 1; Page 677; 11750pp; English.
                                                                  147 AAGCAACGCTTGAAAAAAGGAAA 169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Monahan JE;
                                                                                                 AAAAAAAAAAAAAAAAAAAAAAAA 34
                                                                                                                                                                                                                                                                                                                     Human, prostate cancer, cytostati
pharmacogenomic marker, gene, ss.
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16-MAR-2000; 2000US-189862P.
25-WAY-2000; 2000US-207454P.
09-JUN-2000; 2000US-211314P.
18-JUL-2000; 2000US-21907P.
                                                                                                                                                                                    ABV03810 standard; cDNA; 464
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                                                                                                                                                                                                                                                   (first entry)
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                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens,
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                                                                                                                                                                                                                   ABV03810;
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ABV03810/
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The invention relates to an isolated nucleic acid molecule (I) comprising a nucleotide sequence given in Tables 1-9 (ABV00010-ABV62213) of the specification or its complement. (I) is useful for:
(a) assessing whether a patient is afflicted with prostate cancer;
(b) monitoring the progression of prostate cancer in a patient;
(c) assessing the efficacy of a test compound to inhibit prostate
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Human; prostate cancer; cytostatic; carcinogen; pharmacodyanamic marker;
pharmacogenomic marker; gene; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Novel isolated nucleic acid molecule associated with cancerous state of prostate cells and correlating with presence of prostate cancer, useful for detecting presence of prostate cancer -

    (a) assessing whether a patient is afflicted with prostate cancer;
    (b) monitoring the progression of prostate cancer in a patient;
    (c) assessing the efficacy of a test compound to inhibit prostate cancer in a patient;
    (d) assessing the efficacy of a therapy for inhibiting prostate cancer in a patient;

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    is also useful as a pharmacodyanamic or pharmacogenomic marker.

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                                                                                                                                                                                                                                                   Human prostate expression marker cDNA 43592
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 1; Page 8681-8682; 11750pp; English.
                             147 AAGCAACGCTTGAAAAAAGGAAA 169
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25-WAY-2000; 2000US-207454P.
09-JUN-2000; 2000US-211314P.
18-JUL-2000; 2000US-219007P.
13-DEC-2000; 2000US-255281P.
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TTATTTATTCCCAAATTTTTCTTAAGCAAATATTTCTTTGCTAATCAATAAATTATCAAA 131

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The invention relates to a nucleic acid comprising a sequence of at least 18 bases of a segment of chemically pretreated DNA of genes associated with cell signalling. The activity of the modified sequences of the invention may be described as cytostatic. The object of the invention is to provide the chemically modified DNA of genes associated with cell signalling, as well as oligonucleotides and/or DNA-oligomers for detecting cytosine methylations, as well as a method which is particularly suitable for the diagnosis and/or therapy of genetic and epigenetic parameters of genes associated with cell signalling. The chemically modified DNA provided by the invention is useful for diagnosis and therapy of diseases such as solid tumours and cancer. The sequences
represented in the printed
                                                                     Nucleic acid, useful for diagnosis and therapy of diseases associated with cell signalling e.g. cancer, comprises chemically modified genomic sequences of genes associated with cell signalling -
                                                                                                                                                                                                                                                                                                                                              Chemically treated cell signalling DNA sequence complementary to#45.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             given in records ABL70111-ABL70626 represent chemically pre-treated genomic DNA's of genes associated with cell signalling.
Note: The sequence data for this patent is not represented in the pr specification, but is based on sequence information supplied by the European Patent Office.
                                                                                                                                                                                                                                                                                                                                                                                Cell signalling; cytosine methylation; cell signalling disease;
cancer; tumour; cytostatic; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 10988 BP; 3128 A; 225 C; 2649 G; 4986 T; 0 other;
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                                                                                                                                                                                                                                   ABL70200 standard; DNA; 10988 BP.
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01-SEP-2000; 2000DE-1043826.
                                                                                                                                                                                                                                                                                                          (first entry)
                                                                                                         159 AAAAAAGGAAA 169
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                                                                                                                                          45 AAAAAAAAA 35
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WO200177375-A2 Homo sapiens.

Human; Gene regulation-associated gene; severe combined immunodeficiency; cardiac damage; inflammatory response; Haemophilia; Werner syndrome; asthma; HDR syndrome; congenital heart defect; Saethre-Chotzen syndrome; renal disease; Preeclampsia; cardiac allograft vascular disease; colorectal cancer; thyroid cancer; asophageal cancer; ds; tumour; immunostimulant; cardiant; antiinflammatory; coagulant; antiasthmatic; nephrotropic; gynecological; anti-tumour; immunosuppressive; cytostatic.

Human gene regulation-associated gene oligonucleotide #113.

(first entry)

29-JAN-2002

AAS61158;

AAS61158 standard; DNA; 10988 BP.

AAS61158

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The invention relates to 224 nucleic acid sequences comprising at least

18 bases of a chemically pretreated gene associated with gene regulation
selected from 43 known genes (or complementary sequences). The
chemical pretreatment converts cytosine bases unmethylated at the
5-position to uracil or another bases with hybridisation behaviour
dissimilar to cytosine, to enable analysis of cytosine methylations.
The DNA sequences, oligomers (or sets/arrays) and method are
useful in the diagnosis of diseases (or predisposition to diseases)
associated with gene regulation and in therapy of such diseases,
this are provided. They are especially useful in diagnosis
and therapy of e.g. severe combined immunodeficiency disease, cardiac
disorders, haemophilia, solid tumours and cancer, Werner syndrome,
asthma, HDR syndrome, Saethre-Chotzen syndrome, renal disease.

breadlampsia, graft versus-host disease. The present sequence is a
sequence included in the sequence data for this specification and is
sequence included in the sequence data for this specification and is
Note: The sequence data for this patent did not form part
of the printed specification, but was obtained in electronic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New nucleic acid sequences from chemically modified genes associated with gene regulation, useful for analysing cytosine methylations for diagnosis and therapy of diseases e.g. severe combined immunodeficiency
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 1; SEQ ID No 116; 26pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                       07-APR-2000; 2000DE-1019173.
                                                                                                                                                                                                                                                                                                                                                                    06-APR-2001; 2001WO-EP03968.
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Gaps

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49; Indels

0; Mismatches Score 44.6; Pred. No. 1.

Query Match
Best Local Similarity 60.2%;
Matches 74; Conservative

Length 10988;

DB 24; 1.1;

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132 AGA 134
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human; signal transduction associated gene; cytosine methylation state; CpG island; signal transduction associated disease; solid tumour; cancer; antitumour; cytostatic; mutant; ds.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The present invention relates to chemically modified DNA sequences of signal transduction associated genes. The DNA sequences are chemically modified using a solution of bisulphite, hydrogen sulphite or disclosed are oligonucleotides and/or PNA oligomers for detecting the cytosine methylation state (CpG islands) of these genes, and a method for the diagnosis and/or therapy of genetic and epigenetic parameters of genes associated with signal transduction. The genomic DNA can be obtained from cells or cellular components which contain DNA, e.g. cell lines, biopsies, blood, sputum, stool, urine, cerebral-spinal fluid, tissue embedded in paraffin such as tissue from eyes, intestine, kidney, brain, heart, prostate, lung, breast or liver, histologic object slides, and all their possible combinations. The sequences of the invention are useful for the diagnosis and therapy of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Oligonucleotide for diagnosis and therapy of diseases associated with signal transduction e.g. cancer, comprises chemically modified genomic sequences of genes associated with signal transduction -
                                                                                                                                                                                                                                                                                                         TTATTTATTCCCAAATTTTTCTTAAGCAAATATTTCTTTGCTAATCAATAAATTATCAAA
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                                                                                                                  DB 24; Length 10988;
                                                                    Sequence 10988 BP; 3128 A; 225 C; 2649 G; 4986 T; 0 other;
                                                                                                                                                              49; Indels
                                                                                                                8.4%; Score 44.6; DE 60.2%; Pred. No. 1.1; ive 0; Mismatches
format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
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01-SEP-2000; 2000DE-1043826.
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                                                                                                                Query Match
Best Local Similarity 60.2<sup>3</sup>
Matches 74; Conservative
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diseases associated with signal transduction e.g. solid tumours and cancer. ABK31158-ABK311545 represent chemically pretreated genomic DNA sequences of different genes associated with signal transduction, or their complementary sequences. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   markers for determining the sensitivity of a cancer cell to the anticancer agent TAXOL. Cancer cells can be treated with TAXOL when they are shown to express one of the 242 sensitivity markers or the cells are shown not to express one of the 804 resistance markers. The methods can be used to determine the effectiveness of TAXOL in the treatment of cancer cell growth in an individual. The markers can be used as targets in developing anti-cancer agents such as chemocherapeutic compounds. The markers can also be used as targets in developing treatments for cancer, particularly those cancers which
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  nucleic acid, used as a marker to determine the effectiveness of TAXOL to treat cancer cell growth in individuals -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human; cancer cell marker; TAXOL; cytostatic; tumour; carcinoma;
squamous cell carcinoma; sarcoma; fibrosarcoma; leukaemia;
lymphocytic leukaemia; lymphoma; plasmocytoma; reticulum cell sarcoma;
Hodgkin's disease; glioma; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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                                                                                                                                                                                                                                                                                                                                           DB 24; Length 10988;
                                                                                                                                                                                                                                                                             Sequence 10988 BP; 3128 A; 225 C; 2649 G; 4986 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                            49; Indele
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                                                                                                                                                                                                                                                                                                                                           Score 44.6; DE
Pred. No. 1.1;
0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human cancer agent-sensitive marker #181.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 1; Page 221; 527pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAS60450 standard; cDNA; 425 BP.
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                                                                                                                                                                                                                                                                                                                                       8.4%;
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                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 60.47
Local Similarity 60.47
Local Similarity 60.47
                                                                                                                                                                                                               European Patent Office
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                                                                                                                                                                                                                                                                                                                                 display resistance to agents and exhibit expression of the markers. The anticancer agents developed by the novel method can be used to treat cancer. Probes based on the markers can be used to detect transcripts or genomic sequences corresponding to the markers, in the identification of cells or tissues which mis-express the protein. Cancers which may be targeted include carcinoma (e.g. squamous cell carcinoma), lymphoma, plasmocytoma, reticulum cell sarcoma, Hodgkin's disease and tumours (e.g. glioma). The present sequence is one of the 1046 novel cancer cell markers.
                                                                                                                                                                                                                                                                                                  Human, prostate cancer, cytostatic, carcinogen, pharmacodyanamic marker, pharmacogenomic marker, gene, ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Novel isolated nucleic acid molecule associated with cancerous state of prostate cells and correlating with presence of prostate cancer, useful for detecting presence of prostate cancer -
                                                                                                                                                                                                                                                                   27 TITATATGCTGATTTATGGGTGATTTTGCTTCCTTCTTTATACTTTTATTTCCCAAA
                                                                                                                                                                                                                                      Gaps
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                                                                                                                                                                                                        22; Length 425;
                                                                                                                                                                                                                                     69; Indels
                                                                                                                                                                           Sequence 425 BP; 159 A; 41 C; 28 G; 194 T; 3 other;
                                                                                                                                                                                                                                                                                                                                                                                            147 AAGCAACGCTTGAAAAAGGAAAGTTAGCCCTA 179
                                                                                                                                                                                                                                                                                                                                                                                                                         AAAAAAAAAAAAAAAAAAAAAATTTCCCCCA 163
                                                                                                                                                                                                         Score 44.4; DB Pred. No. 0.48;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human prostate expression marker cDNA 10012.
                                                                                                                                                                                                                                     0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 1; Page 1602; 11750pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ABV10021 standard; cDNA; 494 BP
                                                                                                                                                                                                      ch 8.4%;
1 Similarity 54.9%;
84; Conservative
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16-MAR-2000; 2000US-189862P.
25-MAY-2000; 2000US-207454P.
99-JUN-2000; 2000US-211314P.
18-JUL-2000; 2000US-219007P.
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                                                                                                                                                                                                                      Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                     neuroleptic; antimanic; cerebroprotective; immunomodulatory; antimanic; cerebroprotective; immunomodulatory; anti-microbial; cardiant; cytostatic; antiinflammatory; haemostatic; anticonvulsant; vasotropic; vaccine; gene therapy; anti-sense therapy; neural; reproductive; immuno disorder; immunodeficiency; infection; lymphoma; demyelinating disease; autoimmunity; cancer; inflammation; aneurysm; haemorrhage; Alzheimer's disease; Parkinson's disease; Huntington's disease; Tourette syndrome; multiple sclerosis; meningitis; ischaemia; mania; dementia; obsessive compulsive disorder; viral prophylaxis; developmental disorder; sexually-linked disorder;
                                                                                                selecting a composition for inhibiting prostate cancer in a patient, assessing the prostate cell carcinogenic potential of a compound, determining whether prostate cancer has metastasized in a patient; assessing the aggressiveness or indolence of prostate cancer in a

(a) assessing whether a patient is afflicted with prostate cancer;
(b) monitoring the progression of prostate cancer in a patient;
(c) assessing the efficacy of a test compound to inhibit prostate cancer in a patient;
(d) assessing the efficacy of a therapy for inhibiting prostate cancer in a patient;

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    is also useful as a pharmacodyanamic or pharmacogenomic marker.

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GA, Ebner R, Komatsoulis G;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      secreted protein; diagnosis; neuroprotective; nootropic;
                                                                                                                                                                                                                                                    8.4%; Score 44.4; DB 23; Length 494; 9.5%; Pred. No. 0.5;
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                                                                                                                                                                                                                     Sequence 494 BP; 299 A; 19 C; 21 G; 155 T; 0 other;
                                                                                                                                                                                                                                                                                   51;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human secreted protein gene 49 SEQ ID NO:66.
                                                                                                                                                                                                                                                                  59.5%; Pred. No. 0.5; tive 0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAA26336 standard; cDNA; 664
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98US-0098634.
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                                                                                                                                                                                                                                                                Local Similarity 59.5
nes 75; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 2000-224656/19.
P-PSDB; AAY91401.
                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAGCAA 152
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31-AUG-1998;
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Soppet DR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                     147
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Berlin K;

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Human; tumour suppressor gene; oncogene; antitumour; cytostatic;
cancer; tumour; CpG dinucleotide; single-nucleotide polymorphism; SNP;
cytosine methylation; ds.
                                                                                                                                                                                                                                                                                                                                                                       Tumour suppressor gene derived chemically modified sequence #128
                                                                                                                                                                                                                                                                                                                                 AAS46406 standard; DNA; 6078 BP
                                                                                                                                                                                                        Query Match
Best Local Similarity 52.8%;
Matches 93; Conservative
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06-APR-2000; 2000DE-1019058.
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                                                                                                                                                                                                                                                                                                                                                         18-DEC-2001 (first entry)
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The invention relates to a nucleic acid comprising a sequence of 18 bases, of a segment of chemically pretreated DNA (CP DNA) e.g. with bases, of a segment of chemically pretreated DNA (CP DNA) e.g. with bisulphite, of genes associated with rumour suppression and concogenes having a sequence taken from 536 (actually 533 since numbers 408, 458 and 500 are missing from the sequence listing) sequences complementary to (Sa). The nucleic acid may be a peptide nucleic acid may be a compared nucleic acide polymorphisms and also to be used in an array for analysing diseases associated with CpG dinucleotides e.g. cancers and tumours. The probes can also be used in a method for array for analysing diseases associated with CpG dinucleotides e.g. cancers and tumours. The probes can also be used in a method for array for analysing diseases or the predisposition to specific and/or therapy of existing diseases or the predisposition to specific diseases, by analysing cytosine methylations. The parameters may be compared to another set of genetic and/or epigenetic parameters which are disadvantageous to patients. The present sequence is one of the careful and prodisposition to appear and form tumour suppressor genes and compared sequence derived from tumour suppressor genes and compared sequence of the corresponding odd numbered sequence (e.g. complementary sequence of the corresponding odd numbered sequence (e.g. complementary sequence of the corresponding odd numbered sequence (e.g. complementary sequence of the corresponding odd numbered sequence (e.g. complementary sequence of the corresponding odd numbered sequence (e.g. complementary sequence of the corresponding odd numbered sequence (e.g. complementary sequence of the corresponding odd numbered sequence (e.g. complementary sequence of the corresponding odd numbered sequence (e.g. complementary sequence of the corresponding odd numbered sequence (e.g. complementary sequence and idle is a corresponding odd numbered sequence enterpressor genes and corresponding of the corr
                                                                                                                                                                                                                                                                                                                                                                 Fragments of chemically modified genes associated with tumour suppressor genes and oncogenes, useful in designing primers and probes for analysing diseases associated with cytosine methylation state e.g.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 1; SEQ ID No 128; 27pp; English
07-APR-2000; 2000DE-1019173.
30-JUN-2000; 2000DE-1032529.
01-SEP-2000; 2000DE-1043826.
                                                                                                                                                                                                                         Piepenbrock C,
                                                                                                                                               (EPIG-) EPIGENOMICS AG
                                                                                                                                                                                                                                                                                               WPI; 2001-602752/68.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     is missing)
                                                                                                                                                                                                                     olek A,
   The polynucleotide sequences given in AAA26281 to AAA26336 encode the human secreted proteins given in AAY91346 to AAY91449. The human secreted proteins given in AAY91346 to AAY91449. The human secreted human secreted proteins given in AAY91346 to AAY91449. The human secreted expressed in. Examples of the activities are: neuroprotective; nouroprotective; neuroprotective; nouroleptic; antimanic; cerebroprotective; immunomodulatory; nemostatic; anti-final anti-final and vasotropic. The polynucleotides and proteins may be used to prevent, treat or ameliorate a medical condition, e.g. by protein or gene therapy. Conditions, treatable by the proteins of the invention include neural; reproductive, or immune disorders, especially immunodeficiency, infection, lymphomas, demyelinating diseases, auto-immunities, cancer, general microbial infection, inflammation, aneurysms and haemorrhages. Specific examples include Alzeimer's disease; Parkinson,'s; Huntington's; Tourette syndrome; multiple sclerosis; meningitis; ischaemis; prostate cancer; mania; dementia; cobessistive compulsive disorder and viral prophylaxis. The polynucleotides and proteins can also be used in the detection of disorders associated with the function of the protein, for example, the detection of developmental disorders, sexually-linked disorders of the cardiovascular system. They may also be used as food additives or preservatives. AAA26272 to AAA26280 and AAY91345 are sequences used in the exemplification of the present invention.
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                                  Novel secreted proteins and corresponding DNA molecules that can be used to prevent, treat and diagnose disease in humans, for example, Alzheimer's, cancer, and immune disorders -
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Pred. No. 0.55;
1; Mismatches 82; Indels 0:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 664 BP; 206 A; 138 C; 133 G; 182 T; 5 other;
                                                                                                                                                                                  Claim 1; Page 353; 416pp; English
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4435
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                                                                                                        65 TATACTTTTATTTATTCCCAAATTTTTCTTAAGCAAATATTTCTTTGCTAATCAATAAAT 124
                                                                                                                                          125 TATCAAAAGAAAAAAAAACTGAAAGCAACGCTTGAAAAAAAGGAAAGTTAGCCCTATCGGG
                                                                      ö
                                Query Match
8.4%; Score 44.4; DB 22; Length 6078;
Best Local Similarity 54.4%; Pred. No. 1.1;
Matches 87; Conservative 1; Mismatches 72; Indels 0;
Sequence 6078 BP; 1615 A; 218 C; 1499 G; 2746 T; 0 other;
                                                                                                                                                                                                                                                                                            4374 TATITITIATAATITITAATATITICCAAATITICTACAA 4335
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human immune system associated gene SEQ ID NO: 1110.
                                                                                                                                                                                                                                                      185 TATATTTTGGAAGTTGTAAAATACTACRTGTTCTCTA
                                                                                                                                                                                                                                                                                                                                                                                    ABL33137 standard; DNA; 6078 BP
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                                                                                                                                                                                                                                                                                                                                                                                                                        ABL33137;
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anticancer therapy; carcinogen; antisense inhibition.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ABX47018 standard; cDNA; 236 BP
                                                                                                                                                                                                                                                                                                                                                                                  20; Page 407; 436pp; English.
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ilarity 54.5%;
Conservative (
                                                                                                                                                             14-MAR-2000; 2000US-0189113.
31-MAR-2000; 2000US-0193943.
12-MAY-2000; 2000US-0203772.
                                                                                                          08-DEC-2000; 2000WO-US33311.
                                                                                                                                                                                                       09-JUN-2000; 2000US-0210820
                                                                                                                                                                                                                   21-JUL-2000; 2000US-0220113
                                                                                                                                                                                                                                                                        Deeds J,
                                                                                                                                                                                                                                                                                                 WPI; 2001-367889/38.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Local Similarity
Les 78; Conserv
                                                      WO200142792-A2
                             Homo sapiens.
                                                                                                                                     08-DEC-1999;
21-DEC-1999;
                                                                                                                                                                                                                                                                        Schlegel R,
                                                                                 14-JUN-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The present invention provides a number of human immune system associated genes which are modified by the methylation of cytosines. The sequences can be used in the diagnosis and treatment of immune system disorders, including eye diseases such as retinopathy, neovascular glaucoma and macular degeneration, arteriosclerosis, anaemia, cancer, acute myeloid relukaemia, Alzheimer's disease, Alzheitepsy, neurofibromatosis, rheumatoid arthritis, psoriasis and inflammatory/ulcerative bowel diseases. The present sequence is a gene of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        65 TATACTTTTATTTATTCCCAAATTTTTCTTAAGCAAATATTTCTTTGCTAATAAAAT 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               125 TATCAAAAGAAAAAAACTGAAAGCAACGCTTGAAAAAAGGAAAGTTAGCCCTATCGGG 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Cervical cancer; pre-malignant condition marker; tumourigenesis; CIN; ds; cervical intraepithelial neoplasia; squamous intraepithelial lesions; polymerase chain reaction; PCR; enzyme linked immunosorbent assay; ELISA;
                                                                                                                                                                                                                                                                                                                                                     Nucleic acid comprising fragment of chemically modified gene, useful for diagnosis and treatment of diseases associated with abnormal
Human; immune system disease; cytosine methylation; antiasthmatic; antiansemic; cytostatic; nootropic; nontiansemic; oytostatic; nootropic; neucoprotective; anti-HIV; anticonvulsant; ophthalmologic; antirheumatic; antiarthritic; antidiabetic; antipsoriatic; antinflammatory; cancer; eye disease; arteriosclarosis; anemia; acute myeloid leukaemia; Alzheimer's disease; AlDS; epilepsy; neurofibromatosis; rheumatoid arthritis; psoriasis; bowel disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Match 8.4%; Score 44.4; DB 24; Length 6078; Local Similarity 54.4%; Pred. No. 1.1; Nonservative 1; Mismatches 72: Thiale n.
                                                                                                                                                                                                                                                                                                                                                                                                           Claim 1; SEQ ID NO 1110; 32pp + Sequence Listing; German.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 6078 BP; 1615 A; 218 C; 1499 G; 2746 T; 0 other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            4374 TATTTTTTATTTTTTATTTTTCCAAATTTTCTACAA 4335
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TATATTTTGGAAGTTGTAAAATACTACRTGTTCTCTTCTA 224
                                                                                                                                                                                                                                                                                                   Berlin K;
                                                                                                                                                                                                      02-JUL-2001; 2001WO-EP07537.
                                                                                                                                                                                                                              30-JUN-2000; 2000DE-1032529.
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                                                                                                                                                                                                                                                                                                Piepenbrock C,
                                                                                                                                                                                                                                                                        (EPIG-) EPIGENOMICS AG
                                                                                                                                                                                                                                                                                                                                                                                  cytosine methylation
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                                                                                                                                                  WO200200928-A2
                                                                                                                         Homo sapiens.
                                                                                                                                                                             03-JAN-2002
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                                                                                               gene; ds
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The sequence represents a cervical cancer pre-malignant condition marker.

These markers encode proteins that are over expressed during
tumourigenesis. The proteins and their corresponding nucleic acid
sequences can therefore be used for the diagnosis, prevention and
retained of cervical cancers, particularly cervical intraepithelial
coplasia (CIN) and squamous intraepithelial lesions (SIL). The sequences
may be used as markers in diagnostic assays to detect cancerous
conditions (e.g. by polymerase chain reaction (PCR) or enzyme linked
immunosorbent assay (ELISA), to monitor the efficacy of anticancer
therapies and to identify anticancer or carcinogenic compounds. The level
cervicals of expression of the marker in a patient sample is compared with the normal
level of expression of the marker in a control non-cervical cancer
ample, whereby a significant difference indicates that the patient is
afflicted with cervical cancer or a pre-malignant condition. The
cervical cancers. They may be used in this way for the treatment
cervical intraepithelial neoplasia or squamous intraepithelial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               66
                                                                                                                                                                                                                                                  Cervical cancer protein markers useful for the diagnosis, prevention and treatment of cervical cancers, especially cervical intraepithelial neoplasia or squamous intraepithelial lesions -
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 198 BP; 67 A; 11 C; 10 G; 102 T; 8 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         65;
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(MILL-) MILLENNIUM PREDICTIVE MEDICINE INC
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The invention relates to an isolated nucleic acid molecule (I) comprising a nucleotide sequence given in Tables 1-9 (ABV00010-ABV62213) of the specification or its complement. (I) is useful for:
(a) assessing whether a patient is a afflicted with prostate cancer;
(b) monitoring the progression of prostate cancer in a patient;
(c) assessing the efficacy of a test compound to inhibit prostate selecting a composition for inhibiting prostate cancer in a patient; assessing the prostate cell carcinogenic potential of a compound; determining whether prostate cancer has metastasized in a patient; assessing the aggressiveness or indolence of prostate cancer in a Human; prostate cancer; cytostatic; carcinogen; pharmacodyanamic marker; pharmacogenomic marker; gene; 88. Novel isolated nucleic acid molecule associated with cancerous state of prostate cells and correlating with presence of prostate cancer, useful for detecting presence of prostate cancer cancer in a patient; (d) assessing the efficacy of a therapy for inhibiting prostate cancer is also useful as a pharmacodyanamic or pharmacogenomic marker. ö / Match 8.3%; Score 43.8; DB 23; Length 323; Local Similarity 53.3%; Pred. No. 0.62; Local Suniarity 0; Mismatches 79; Indels 0; Sequence 323 BP; 109 A; 58 C; 34 G; 120 T; 2 other; Human prostate expression marker cDNA 60987. (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC. Claim 1; Page 11593; 11750pp; English. 167 AATGTTAGTGTGAAATGACAAA 189 147 AAGCAACGCTTGAAAAAGGAAA 169 Endege WO, Monahan JE; 멾 2000US-201454P. 2000US-211314P. 2000US-219007P. ABV60996 standard; cDNA; 323 20-FEB-2001; 2001WO-US05171 2000US-189862P 2000US-255281P (first entry) WPI; 2001-662795/76. WO200160860-A2. in a patient; ношо варіепв. 13-DEC-2000; 17-FEB-2000; 25-MAY-2000; Schlegel R, 09-JUN-2000; 23-AUG-2001. 16-MAR-2000; 13-SEP-2002 ABV60996; Query Match patient Matches RESULT 34 (e) (H) ÐĐ ABV60996 ઠે 유 ઠે factation or muscle and far depolition designated LMFD), derived from cattle, and the LMFD nucleic acid can specifically hybridise to a second nucleic acid molecule comprising any of 15112 nucleocide can equences, appearing as ABX4886-ABX49947, or complements of them. Also included are; (1) a transformed cell having a nucleic acid comprising an LMFD nucleic acid linked to a promoter and a 3 non-cranslated sequence that functions in the cell to cause termination of translated sequence that functions in the cell to cause termination of transcription and addition of polyadenylated ribonucleotides to a 3 and molecule; and (2) determining a level or pattern of a molecule in a bovine cell or tissue comprising; (a) incubating a marker nucleic acid (comprising any of the 15112 nucleic acid sequences or its complement or fragment) with a complementary nucleic acid and the complementary nucleic acid and the complementary nucleic acid and the complementary nucleic acid and the complementary nucleic acid and the complementary nucleic acid is predictive of the level or pattern of the LMFD nucleic acid is used for determining a level or pattern of the LMFD nucleic acid is used for determining a level or pattern of the LMFD nucleic acid is used for determining a level or pattern of complementary nucleic acid is used for determining a level or pattern of the LMFD nucleic acid is used for determining a level or pattern of constructs for use in cattle seme expression, or for genetically warm for constructs for use in cattle sequence is one of the 1512 bovine The invention relates to a purified nucleic acid molecule associated with 86 Bovine; ss; EST; expressed sequence tag; lactation; LMFD; muscle deposition; fat deposition; genome mapping; gene identification; gene analysis; cattle breeding. Bovine EST associated with lactation/muscle/fat deposition #12183 LMFD EST (expressed sequence tag) nucleic arine.

Note: The present sequence was not shown in the specification but ö New nucleic acid associated with lactation, and muscle and fat deposition, useful for genome mapping, gene identification and analysis, cattle breeding, or for genetically improving cattle Score 43.8; DB 25; Length 236; Pred. No. 0.56; Indela segdata.uspto.gov/seguence.html?DocID=20020137139. Sequence 236 BP; 63 A; 13 C; 23 G; 137 T; 0 other; 62; Warren WC; 0; Mismatches Claim 2; SEQ ID No 12183; 245pp; English. Tao N, 8.3%; 12-JAN-1999; 99US-115707P. 24-SEP-2001; 2001US-0960352. (first entry) Byatt JC, Mathialagan N, 81; Conservative (BYAT/) BYATT J C. (MATH/) MATHIALAGAN N. WPI; 2003-110599/10. (TAON/) TAO N. (WARR/) WARREN W C. Local Similarity US2002137139-A1. 21-FEB-2003 26-SEP-2002. Bos Taurus. Query Match Best Loca Matches

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The invention relates to human polynucleotides (AAI79941-AAI93841) and the encoded proteins (AA000010-AA013910) that exhibit activity elating to cytokine, cell proliferation or cell differentiation or which may induce production of other cytokines in other cell populations. The polymptocleotides and polypeptides are useful in gene therapy, vaccines or peptide therapy. The polypeptides have various cytokine-like activities, e.g. stem cell growth factor activity, heematopoiesis regulating activity, tissue growth factor activity, immunomodulatory activity and activity, and may be useful in the diagnosis and/or treatment of cancer, leukaemia, nervous system disorders, arthritis and
                                   TTATACTITITATICCCAAATITITICTIAAGCAAATATITICTTIGCTAATCAATAAA 123
                                                                     Human, cytokine, cell proliferation, cell differentiation, gene therapy, vaccine; peptide therapy, stem cell growth factor; haematopoiesis; tissue growth factor; immunomodulatory; cancer; leukaemia; nervous system disorders; arthritis; inflammation; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
Isolated nucleic acids and polypeptides, useful for preventing diagnosing and treating e.g. leukaemia, inflammation and immune disorders -
                                                                                                         124 TTATCAAAAAAAAAAAACTGAAAGCAACGCTTGAAAAAAGGAAAGTT 172
                                                                                                                                          136 CCCCCAAAAAAAAAAATTTTTCCCCCCCAAAAAAATTTT 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 1; SEQ ID NO 10923; 1399pp + Sequence Listing; English.
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                                                                                                                                                                                                                                                                                                                                              Human polynucleotide SEQ ID NO 10923.
                                                                                                                                                                                                                                    AAI90863 standard; cDNA; 378
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Tang YT, Liu C, Drmanac RT
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18-MAY-2000; 2000US-0577409.
                                                                                                                                                                                                                                                                                                        (first entry)
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P-PSDB; AAO10932.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          inflammation.
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                                 64
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The invention relates to human polynucleotides (AAI79941-AAI93841) and the encoded proteins (AA000010-AA013910) that exhibit activity elating to cytokine, cell proliferation or cell differentiation or which may induce production of other cytokines in other cell populations. The polynucleotides and polypeptides are useful in gene therapy, vaccines or peptide therapy. The polypeptides have various cytokine-like activities, e.g. stem cell growth factor activity, haematopoiesis regulating activity, tissue growth factor activity, immunomodulatory activity and activity and may be useful in the diagnosis and/or
                                     63 ITTATACTTTTATTCCCAAATTTTTCTTAAGCAAATATTTCTTTGCTAATCAATA 122
120 TGGTCTATCTTAATTTCTCTCAGTAAAATTTTGTGGTTTTTCTCCATAGAATTCTTACACA 179
                                                                        Human, cytokine, cell proliferation, cell differentiation, gene therapy, vaccine, peptide therapy, stem cell growth factor, haematopoiesis, tissue growth factor; immunomodulatory; cancer; leukaemia; nervous system disorders; arthritis; inflammation; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       treatment of cancer, leukaemia, nervous system disorders, arthritis and inflammation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Isolated nucleic acids and polypeptides, useful for preventing diagnosing and treating e.g. leukaemia, inflammation and immune
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                                                                                                              123 ATTATCAAAAGAAAAAAAACTGAAAGCAACGCTTGAAAAAAGGAAA 169
                                                                                                                                                   Claim 1; SEQ ID NO 8655; 1399pp + Sequence Listing; English.
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                                                                                                                                                                                                                                                                                                                                                           Human polynucleotide SEQ ID NO 8655.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Tang YT, Liu C, Drmanac RT;
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18-MAY-2000; 2000US-0577409.
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P-PSDB; AAO08664.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens.
                                                                                                                                                                                                                                                                                                                        06-NOV-2001
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Match 8.3%; Score 43.8; DB 22; Length 378; Local Similarity 53.9%; Pred. No. 0.64; es 90; Conservative 0; Mismatches 77; Indels 0.

Query Match Best Loca Matches

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The invention relates to a nucleic acid comprising a sequence (I) of at least 18 bases in length of a segment of chemically pre-treated genomic DNA which has any one of the sequences of (ARX3319-ARX3403) or its complement. Also included are an oligomuclectide or peptide nucleic acid (or set thereof) of at least 9 nucleotides which hybridises to (I), probes for detecting cytosine methylation or singlenuclectide polymorphisms (SNP) in (I), a marray of oligomers or peptide nucleic acids for analysing diseases associated with the nucleotide polymorphisms (SNP) in (I), a marray of oligomers or peptide nucleic acids for analysing diseases associated with the corporation grading, staging, treatment and/or diagnosis of differentiation, grading, staging, treatment and/or diagnosis of differentiation, grading, staging, treatment and/or diagnosis of astrocytomas, or the predisposition to astrocytomas by analysing growing methylations, involves obtaining a biological sample containing genomic DNA, extracting the genomic DNA, entracting the genomic DNA, entracting the genomic DNA, entracting the genomic DNA amplificates at the 5-position, in the genomic DNA sample, to uracil or another base which is dissimilar to cytosine in terms of hybridisation cancher base which is dissimilar to cytosine positions by reference to amplificates carry a detectable label. The method further involves density methylation status of one or more cytosine positions by using a nalysing methylation status of the cytosine positions by reference to one or more data sets. The genomic DNA is chemically treated by using a biallibite, hydrogen sulphite or disulphite. The amplification
                                                Human, ds; astrocytoma, cytostatic; staging; cysteine methylation; CpG; bisulphite; brain tissue; MALDI; ESI; electron spray mass spectrometry; matrix assisted laser desorption/ionization mass spectrometry.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Novel chemically modified genomic DNA sequences, useful in the characterisation, classification, differentiation, grading, staging, treatment and/or diagnosis of astrocytomas or predisposition to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human DNA for staging of Astrocytomas #4.
                                                                                                                                                    147 AAGCAACGCTTGAAAAAGGAAA 169
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                                                                                                                                                                                                                                                                                                                                    ABK33925 standard; DNA; 9884 BP
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01-SEP-2000; 2000DE-1043826.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              66
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human, tumour suppressor gene, oncogene, antitumour, cytostatic,
cancer, tumour, CpG dinucleotide, single-nucleotide polymorphism, SNP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              40 TIAIGGGIGATITICCTICCTICTITATACTITITATICCCAAATTITITCTIAAGCA
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                                                                                                                                                                                                                                                                                                                                                              Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 9884 BP; 2483 A; 226 C; 2338 G; 4837 T; 0 other;
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ID AAS46793 Btandard; DNA; 56153
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07-APR-2000; 2000DE-1019173.
30-JUN-2000; 2000DE-1032529.
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Best Local 8
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Homo sapiens.
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Dases, of a segment of chemically pretreated DNA (CP DNA) e.g. with bisulphite, of genes associated with tumour suppression and oncogenes having a sequence taken from 536 (actually 533 since numbers 408, 458 and 500 are missing from the sequence listing) sequences complementary to (58). The nucleic acid may be a peptide nucleic acid-oligomer (PNA) of at least 9 nucleotides and may for many part of a set of probes for detecting the cytosine methylation state and/or single nucleotide polymorphisms and also to be used in an array for analysing diseases associated with CpG dinucleotides e.g. cancars and tumours. The probes can also be used in a method for ascertaining genetic and/or epigenetic parameters for the diagnosis and/or therapy of existing diseases or the predisposition to specific diseases, by analysing cytosine methylations. The parameters may be compared to another set of genetic and/or epigenetic parameters may be compared to another set of genetic and/or epigenetic parameters which are disadvantageous to patients. The present sequence is one of the case and cancers and cancers and cancers and cancers and patients. The present sequence is one of the case and cancers and cancers and cancers and cancers and cancers and cancers and cancers and cancers and cancers and cancers and cancers and cancers and cancers are the present sequence is one of the case and cancers and cancers and cancers and cancers and cancers and cancers and cancers and cancers and cancers and cancers and cancers and cancers and cancers and cancers and cancers and cancers and cancers and cancers and cancers and cancers and cancers and cancers and cancers and cancers and cancers and cancers and cancers and cancers and cancers and cancers and cancers and cancers and cancers and cancers and cancers and cancers and cancers and cancers and cancers and cancers and cancers and cancers and cancers and cancers and cancers and cancers and cancers and cancers and cancers and cancers and cancers and cancers and cancers and cancers and cancers and 
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   63 ITTATACTITIATITCCCAAATITITCTTAAGCAAATATITCTTIGCTAATCAATAA 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TCTTTGAGCAGGAAAGAAAGCAGTCACCCTCTCTTCCATGACAACAACCCATGACCGG 302
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       183 GGTATATTTTGGAAGTTGTAAAATACTACRIGTTCTCTTCTAAGTCCCACTCCTCTTTT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
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Best Local Similarity 47.5%;
Matches 126; Conservative
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87 ITTTTCTTAAGCAAATATTTCTTTGCTAATCAATAAATTATCAAAAGAAAAAAACTGA 146
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                prostate cells and correlating with presence of prostate cancer, useful for detecting presence of prostate cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   assessing the efficacy of a therapy for inhibiting prostate cancer
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The invention relates to an isolated nucleic acid molecule (I) compris a nucleotide sequence given in Tables 1-9 (ABV00010-ABV62213) of the specification or its complement. (I) is useful for:
(a) assessing whether a patient is afflicted with prostate cancer;
(b) monitoring the progression of prostate cancer in a patient;
(c) assessing the efficacy of a test compound to inhibit prostate
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    is also useful as a pharmacodyanamic or pharmacogenomic marker.

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0; Mismatches
                                                                                                                                                                                                                                                                                                                                                              (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
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25-MAY-2000; 2000US-207454P.
09-JUN-2000; 2000US-211314P.
18-JUL-2000; 2000US-219007P.
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86

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12-MAY-2000; 2000US-0203791.
09-JUN-2000; 2000US-0210600.
21-JUL-2000; 2000US-0220114.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          The present invention provides a number of human immune system associated genes which are modified by the methylation of cytosines. The sequences can be used in the diagnosis and treatment of immune system disorders, including eye diseases such as retinopathy, neovascular glaucoma an macular degeneration, arreriosclerosis, anaemia, cancer, acute myeloid leukaemia, Alzheimer's disease, Alzheimer's disease, PIDS, epilepsy, neurofibromatosis, rheumatoid arthritis, psoriasis and inflammatory/ulcerative bowel diseases. The present sequence is a gene of the invention.
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                                                                                                                                                                                                                                                                                                                                    Nucleic acid comprising fragment of chemically modified gene, useful for diagnosis and treatment of diseases associated with abnormal
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 24; Length 6590;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              59; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 1; SEQ ID NO 1449; 32pp + Sequence Listing; German
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14-MAR-2000; 2000US-0189315.
                                                                                                                                            30-JUN-2000; 2000DE-1032529.
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                                                                                                    02-JUL-2001; 2001WO-EP07537.
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Matches 79; Conservative
                                                                                                                                                                                                                                                   Piepenbrock C,
                                                                                                                                                                                                           (EPIG-) EPIGENOMICS AG
                                                                                                                                                                                                                                                                                                                                                                               cytosine methylation
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                                                             03-JAN-2002
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HE KEY SON WAS BY SEN BY SEN BY SEN BY SEN BY SEN BY SEN BY SEN BY SEN BY SEN BY SEN BY SEN BY SEN BY SEN BY SEN BY SEN BY SEN BY SEN BY SEN BY SEN BY SEN BY SEN BY SEN BY SEN BY SEN BY SEN BY SEN BY SEN BY SEN BY SEN BY SEN BY SEN BY SEN BY SEN BY SEN BY SEN BY SEN BY SEN BY SEN BY SEN BY SEN BY SEN BY SEN BY SEN BY SEN BY SEN BY SEN BY SEN BY SEN BY SEN BY SEN BY SEN BY SEN BY SEN BY SEN BY SEN BY SEN BY SEN BY SEN BY SEN BY SEN BY SEN BY SEN BY SEN BY SEN BY SEN BY SEN BY SEN BY SEN BY SEN BY SEN BY SEN BY SEN BY SEN BY SEN BY SEN BY SEN BY SEN BY SEN BY SEN BY SEN BY SEN BY SEN BY SEN BY SEN BY SEN BY SEN BY SEN BY SEN BY SEN BY SEN BY SEN BY SEN BY SEN BY SEN BY SEN BY SEN BY SEN BY SEN BY SEN BY SEN BY SEN BY SEN BY SEN BY SEN BY SEN BY SEN BY SEN BY SEN BY SEN BY SEN BY SEN BY SEN BY SEN BY SEN BY SEN BY SEN BY SEN BY SEN BY SEN BY SEN BY SEN BY SEN BY SEN BY SEN BY SEN BY SEN BY SEN BY SEN BY SEN BY SEN BY SEN BY SEN BY SEN BY SEN BY SEN BY SEN BY SEN BY SEN BY SEN BY SEN BY SEN BY SEN BY SEN BY SEN BY SEN BY SEN BY SEN BY SEN BY SEN BY SEN BY SEN BY SEN BY SEN BY SEN BY SEN BY SEN BY SEN BY SEN BY SEN BY SEN BY SEN BY SEN BY SEN BY SEN BY SEN BY SEN BY SEN BY SEN BY SEN BY SEN BY SEN BY SEN BY SEN BY SEN BY SEN BY SEN BY SEN BY SEN BY SEN BY SEN BY SEN BY SEN BY SEN BY SEN BY SEN BY SEN BY SEN BY SEN BY SEN BY SEN BY SEN BY SEN BY SEN BY SEN BY SEN BY SEN BY SEN BY SEN BY SEN BY SEN BY SEN BY SEN BY SEN BY SEN BY SEN BY SEN BY SEN BY SEN BY SEN BY SEN BY SEN BY SEN BY SEN BY SEN BY SEN BY SEN BY SEN BY SEN BY SEN BY SEN BY SEN BY SEN BY SEN BY SEN BY SEN BY SEN BY SEN BY SEN BY SEN BY SEN BY SEN BY SEN BY SEN BY SEN BY SEN BY SEN BY SEN BY SEN BY SEN BY SEN BY SEN BY SEN BY SEN BY SEN BY SEN BY SEN BY SEN BY SEN BY SEN BY SEN BY SEN BY SEN BY SEN BY SEN BY SEN BY SEN BY SEN BY SEN BY SEN BY SEN BY SEN BY SEN BY SEN BY SEN BY SEN BY SEN BY SEN BY SEN BY SEN BY SEN BY SEN BY SEN BY SEN BY SEN BY SEN BY SEN BY SEN BY SEN BY SEN BY SEN BY SEN BY SEN BY SEN BY SEN BY SEN BY SEN BY SEN BY SEN BY SEN BY SEN B
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       84
                                                                                                                                                                                                                                                                                                                                          The invention relates to novel genes (AAH68727-AAH71383) associated with cervical cancer with cytostatic activity. The nucleic acids and encoded polypeptides are useful: to assess if a patient is affilicted with cervical cancer or has a pre-malignant condition; to monitor the progression of cervical cancer or a premalignant condition in a patient; and to select and/or assess the efficacy of a compound or therapy for inhibiting cervical cancer in a patient. The nucleic acids may also be
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bovine; 88; EST; expressed sequence tag; lactation; LMFD; muscle deposition; fat deposition; genome mapping; gene identification; gene analysis; cattle breeding.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  124 TTATCAAAAGAAAAAAAACTGAAAGCAACGCTTGAAAAAAGGAAAGTTAGCCCTATCGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            64 TIATACTITIATITATICCCAAATTITICTTAAGCAAATATTICTTIGCTAATAAA
                                                                                                                                                                                       New isolated nucleic acid for diagnosing and treating cervical cancer and for assessing and detecting compounds for treating the cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 43.4; DB 22; Length 300;
Pred. No. 0.75;
0; Mismatches 106; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 300 BP; 81 A; 27 C; 20 G; 143 T; 29 other;
(MILL-) MILLENNIUM PREDICTIVE MEDICINE INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GTATATTTTGGAAGTTGTAAATA 207
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GTTTTTTAAGGGAAAAAAAAAA 228
                                                                                                                                                                                                                                                                                   Claim 1; Page 309; 1051pp; English
                                                              Berger A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ABX46053 standard; cDNA; 424
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               8.2%;
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11-JAN-2000; 2000US-0480902.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Similarity 48.0 98; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         useful for gene therapy.
                                                          Schlegel R, Deeds J,
                                                                                                                         WPI; 2001-375006/39.
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Human prostate expression marker cDNA 4390
                                                                                                                                                               WO200160860-A2
                                                                                                                                                                                                                                                                                                  1.7-FEB-2000; 2
16-MAR-2000; 2
25-MAY-2000; 2
09-JUN-2000; 2
                                                                                                                 Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         in a patient;
                                                                                                                                                                                                                                                                                                                                                                                                                         13-DEC-2000;
                                                                                                                                                                                                           23-AUG-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              셤
                                                                                                                                                                                                                                                                                                              The invention relates to a purified nucleic acid molecule associated with lactation or muscle and fat deposition (designated LMFD), derived from cattle, and the LMFD nucleic acid can specifically hybridise to a second nucleic acid molecule comprising any of 15112 nucleotide sequences, appearing as ABX34836-ABX49947, or complements of them. Also included are; (1) a transformed cell having a nucleic acid comprising an LMFD nucleic acid linked to a promoter and a 3' nontranslated sequence that functions in the cell to cause termination of transcription and addition of polyadenylated fibonucleotides to a 3' end of the mana man addition of polyadenylated fibonucleotides to a 3' end of the mana man addition of the 1512 nucleic acid sequences or its complement or fragment) with a complementary nucleic acid molecule obtained from the bovine cell or tissue, where hybridisation between the marker nucleic acid and the complementary nucleic acid molecule. Complementary nucleic acid and the complementary nucleic acid molecule. The molecule, and (b) detecting the level or pattern of the complementary nucleic acid is predictive of the level or pattern of the complementary nucleic acid is used for determining a level or pattern of the molecule in a bovine cell or tissue. It is useful for genome of a molecule in a bovine cell or tissue. It is useful for genome complements acid is used for determining a level or pattern of the molecule in a bovine cell or tissue. It is useful for genome of constructs for use in cattle gene expression, or for genetically improving cattle. The present sequence is one of the 1512 bovine and malysis, the constructs for mapping acid and the acid and the acid as and analysis, the constructs for mapping acid and the acid and the acid and the acid and the acid and the acid and the acid and the acid and the acid as acid as acid as acid as acid as acid as acid as acid as acid as acid as acid as acid as acid as acid as acid as acid as acid as acid as acid as acid as acid as acid as acid as acid as acid as 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      64 TIATACTITIAITITATICCCAAATITITICTITAAGCAAAIATITCTITGCTAATCAATAAA 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  124 TTATCAAAAGAAAAAAAACTGAAAGCAACGCTTGAAAAAAAGGAAAGTTAGCCCTATCGG 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The present sequence was not shown in the specification but otained in electronic format from the USPTO web site:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                   New nucleic acid associated with lactation, and muscle and fat deposition, useful for genome mapping, gene identification and analysis, cattle breeding, or for genetically improving cattle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 43.4; DB 25; Length 424; Pred. No. 0.83;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1; Mismatches 112; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            184 GTATATTTTGGAAGTTGTAAAATACTACRTGTTCTCTTCTAAG 226
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          190 ATTITAAATATITGITTAAAATATAAAAAAAAAAAATATTATAAG 232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            segdata.uspto.gov/sequence.html?DocID=20020137139.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 424 BP; 228 A; 7 C; 32 G; 157 T; 0 other
                                                                                            Warren WC;
                                                                                                                                                                                                                                                                            Claim 2; SEQ ID No 11218; 245pp; English.
                                                                                            Tao N,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Match 8.2%;
Local Similarity 49.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ABV04399 standard; cDNA; 431
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 was obtained in electronic
                                                                                         Mathialagan N,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best Local Similally ....
Matches 110; Conservative
(MATH/) MATHIALAGAN N.
                        (TAON/) TAO N.
(WARR/) WARREN W C.
                                                                                                                                       WPI; 2003-110599/10
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                                                                                            Byatt JC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 43
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(a) assessing whether a patient is afflicted with prostate cancer;
(b) monitoring the progression of prostate cancer in a patient;
(c) assessing the efficacy of a test compound to inhibit prostate cancer in a patient;
(d) assessing the efficacy of a therapy for inhibiting prostate cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               132
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Human, prostate cancer, cytostatic, carcinogen, pharmacodyanamic marker, pharmacogenomic marker, gene, ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                selecting a composition for inhibiting prostate cancer in a patient, assessing the prostate cell carcinogenic potential of a compound; determining whether prostate cancer has metastasized in a patient;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Novel isolated nucleic acid molecule associated with cancerous state of prostate cells and correlating with presence of prostate cancer, useful for detecting presence of prostate cancer -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      determining whether prostate cancer has metastasized in a patient; assessing the aggressiveness or indolence of prostate cancer in a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                28 ITATATGCTGATTTATGGGTGATTTTGCTTCCTTTTATACTTTTATTTTATTCCCAAAT
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    is also useful as a pharmacodyanamic or pharmacogenomic marker.

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2.1%; Pred. No. 0.83;
ve 0; Mismatches 68; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 431 BP; 139 A; 63 C; 34 G; 114 T; 81 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Schlegel R, Endege WO, Monahan JE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 1; Page 762; 11750pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        148 AGCAACGCTTGAAAAAAGGAAA 169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAAAAAAAAAAAAAAA 50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ABX44170 standard; cDNA; 380 BP
                                                                                                                                                                                                                                                                                                                                                                          ; 2000US-183319P.
; 2000US-189862P.
; 2000US-207454P.
; 2000US-211314P.
; 2000US-219007P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2000US-255281P
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 2001-662795/76.
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Bovine; 88; EST; expressed sequence tag; lactation; LMFD; muscle deposition; fat deposition; genome mapping; gene identification; gene analysis; cattle breeding.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Note: The present sequence was not shown in the specification but was obtained in electronic format from the USPTO web site:
                     Bovine BST associated with lactation/muscle/fat deposition #9335.
                                                                                                                                                                                                                                                                                                  New nucleic acid associated with lactation, and muscle and fat deposition, useful for genome mapping, gene identification and
                                                                                                                                                                                                                                                                                                                deposition, useful for genome mapping, gene identification and analysis, cattle breeding, or for genetically improving cattle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 380 BP; 154 A; 22 C; 46 G; 158 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   segdata.uspto.gov/sequence.html?DocID=20020137139.
                                                                                                                                                                                                                                                                                                                                              Claim 2; SEQ ID No 9335; 245pp; English.
                                                                                                                                                                      12-JAN-1999; 99US-115707P.
                                                                                                                                                24-SEP-2001; 2001US-0960352.
21-FEB-2003 (first entry)
                                                                                                                                                                                                                                                          Byatt JC, Mathialagan N,
                                                                                                                                                                                                   BYATT J C.
MATHIALAGAN N.
                                                                                                                                                                                                                                                                               WPI; 2003-110599/10.
                                                                                                                                                                                                                                    (WARR/) WARREN W C.
                                                                                                        US2002137139-A1.
                                                                                                                            26-SEP-2002.
                                                                                   Bos Taurus.
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Warren WC;

Tao N,

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(b) any one of 115 polynucleotide sequences (ABV83558-ABV83672);
(c) a molecule that selectively hybridizes to (a) or (b);
(d) a molecule that selectively hybridizes to (a) or (b);
(d) a molecule that selectively hybridizes to (a) or (b);
(e) the breast specific nucleic acid molecules, polypeptides and antibodies are useful for identifying, diagnosing, monitoring, staging, imaging and treating breast cancer and non-cancerous disease states in breast tissue. They are also useful for producing transgenic animals and cells and producing engineered breast tissue for treatment and research. The transgenic animals are useful as animal model systems used in elaborating
             109 TTTTTTTTTATAATATTTTTCAAATTTAAAAATATAATTGTTTAAAATTTTTT 168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     the biological function of the polypeptides, studying conditions and/or disorders associated with aberrant expression and in screening for compounds effective in ameliorating the conditions. The polynucleotides
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human; breast; cytostatic; cancer; transgenic; gene therapy; vaccine;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New isolated breast specific nucleic acid molecules and polypeptides, useful for identifying, diagnosing, monitoring, staging, imaging and treating breast cancer and non-cancerous disease states in breast
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gapa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Cafferkey R;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The invention relates to human breast specific nucleic acids (I)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       8.2%; Score 43.2; DB 24; Length 430;
llarity 60.0%; Pred. No. 0.93;
Conservative 0; Mismatches 48; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (a) a sequence encoding any one of 95 protein sequences (ABP66614-ABP66708);
Hu P, Recipon H, Karra K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 430 BP; 135 A; 97 C; 103 G; 95 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 are useful for gene therapy and in vaccines.
                                                                                                                                                                                                                                  Human breast specific gene SEQ ID NO 87.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 1; Page 193-194; 254pp; English.
                                                                       169 AAAAAAATTTAAAAAAAAAAAAA 192
                                         147 AAGCAACGCTTGAAAAAGGAAAG
                                                                                                                                              BP.
                                                                                                                                             ABV83644 standard; cDNA; 430
                                                                                                                                                                                                                                                                                                                                                                                              14-FEB-2002; 2002WO-US04284.
                                                                                                                                                                                                                                                                                                                                                                                                                             L5-FEB-2001; 2001US-268999P
                                                                                                                                                                                                     (first entry)
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Liu C;
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Matches 72; Conserv
                                                                                                                                                                                                                                                                                                                                      WO200266605-A2.
                                                                                                                                                                                                                                                                                                           Homo sapiens.
                                                                                                                                                                                                       06-DEC-2002
                                                                                                                                                                                                                                                                                                                                                                   29-AUG-2002.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              comprising:
                                                                                                                                                                          ABV83644;
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63; Indele

8.2%; Score 43.2; DE 56.2%; Pred. No. 0.9; iive 0; Mismatches

81; Conservative

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Local Similarity

Best Loca Matches

Query Match

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Search completed: February 14, 2004, 14:10:12 Job time : 285 secs

Sequence 36, Ap Sequence 38, Ap Sequence 36, Ap Sequence 38, Ap	4 4		59,	ω α	9 4	9 7	, , ,	idei	,556	ili	000	20.40	, 0, 0	000	4.0,	207	12	120	170	64	9	4 6	Š.	ì.	i	18	in	1,8	17.	96	10	100
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Ltd.		.ime 71 Seconds ignments) .llion cell updates/sec		jagaggettetgag 529			1139956					*. • * * * *		chance to have a result being printed,		Description	2,	9, 1	89,4	i i i	199	(A (A	24,		, o	4	'n'n	99	1,	7 16	equence 23	Sequence 10, Appl Sequence 12, Appl Sequence 12, Appl
GenCore version 5.1.6 ht (c) 1993 - 2004 Compugen Ltd.	ch, using sw model	, 2004, 13:57:05; Search time 71 Seconds (without alignments) 3288.615 Million cell updates/		tagtcgttcttggagagggcttctgag S	NUC 0 , Gapext 1.0	gs, 220691566 residues		. 00000000	Match 0% Match 100%	TIPE TOO BUILDING	acents NA:* 	_//prodate/2/lna/5A_COMB.seq:- _6/prodate/2/lna/6A_COMB.seq:* _6/prodate/2/lna/6B_COMB.seq:* _6/prodate/2/lna/6P_COMB.seq:*	_o/prodata/2/ina/backfiles1.seq:* _6/ptodata/2/ina/backfiles1.seq:*	of results predicted by chance to have a qual to the score of the result being print as of the rotal score distribution	SUMMARIES	DB ID	1 US-07-867-106-2 Sequence 2,	4 US-09-904-615-66 Sequence 66, 1 US-08-703-947-1 Sequence 1,	4 US-09-489-847-89 Sequence 89, 4 US-09-187-999-14 Sequence 14.	2 US-08-446-855A-1 Sequence 1,	4 US-09-904-615-66 Sequence 56,	3 US-09-475-316A-20 Sequence 20, 4 US-09-149-476-208 Sequence 206	4 US-09-149-476-24 Sequence 24,	3 US-08-800-929A-3 Sequence 3,	4 US-09-61/-053A-3 Sequence 3, 3 US-08-545-196B-10 Sequence 10,	3 US-08-545-196B-12 Sequence 12	4 US-09-820-005-3, Sequence 3, 4 US-09-410-464-5 Sequence 5,	4 US-09-149-476-66 Sequence 66,	4 US-09-221-013A-7 Sequence 7,	4 US-09-601-198-165 Sequence 169 4 US-08-916-4218-1 Sequence 1,	4 US-09-369-247-23 Sequence 23	3 US-08-545-196B-10 Sequence 12, 3 US-08-545-196B-12 Sequence 12,
version - 2004	search, using sw	14, 2004, 13:57:05 ; Search time 71 Seconds (without alignments) 3288.615 Million cell updates/		tagtcgttcttggagagggcttctgag S	Gapext	segs, 220691566	satisfying chosen parameters:	ngth: 0 sngth: 200000000	Match Match first	הדפרדות דידפר דרכ פתוווומדידנפ	¥	<pre>. /cgnz_6/ptodata/2/lna/6A_COMB.seq: . /cgnz_6/ptodata/2/lna/6A_COMB.seq:* . /cgnz_6/ptodata/2/lna/6B_COMB.seq:* . /cgnz_6/ptodata/2/lna/6B_COMB.seq:* . /cgnz_6/ptodata/2/lna/6B_COMB.seq:*</pre>	. /cgn2_6/ptodata/2/ina/bac	umber of results predicted by chance to have a or equal to the score of the result being print natural veis of the rotal score distribution	SUMMARIES	Length DB ID	5852 1 US-07-867-106-2 Sequence 2,	.4 664 4 US-09-904-615-66 Sequence 66, .0 2672 1 US-08-703-947-1 Sequence 1,	.9 1342 4 US-09-489-847-89 Sequence 89, 6 1544 4 US-09-187-999-14	.5 8920 2 US-08-446-855A-1 Sequence 1,	.5 664 4 US-09-904-615-66 Sequence 66,	.4 873 3 US-09-475-316A-20 Sequence 20, .3 1378 4 US-09-149-476-208 Sequence 200	.3 2323 4 US-09-149-476-24 Sequence 24,	.3 5232 3 US-03-212-3/11-3 Sequence 3,	.3 5232 4 US-U9-51/-U53A-3 Sequence 3, .2 1582 3 US-08-545-196B-10 Sequence 10,	2 1582 3 US-08-545-196B-12 Sequence 12	.z 18853 4 US-09-820-005-3 .1 5656 4 US-09-410-464-5 Sequence 5,	.1 732 4 US-09-149-476-66 Sequence 66,	.1 3828 4 US-09-221-013A-7 Sequence 7,	.1 4344 4 US-09-601-198-165 Sequence 16: .1 1664976 4 US-08-916-421B-1 Sequence 1,	.0 1492 4 US-09-369-247-23 Sequence 23	US-08-545-1968-10 Sequence 10, US-08-545-1968-12 Sequence 12,
GenCore version (c) 1993 - 2004	wa guisu ,	, 2004, 13:57:05; Search time 71 Seconds (without alignments) 3288.615 Million cell updates/	US-10-027-632-1 core: 529	l catggtgatgctgtagtcgttcttggagagggcttctgag S				DB seq length: 0 DB seq length: 2000000000	Match Match	3 ,	¥		. /cgn2_6/ptodata/2/ina/bac	e number of results predicted by chance to have a han or equal to the score of the result being print by analysis of the rotal score distribution	SUMMARIES	ery tch Length DB ID	2 9.3 5852 1 US-07-867-106-2 Sequence 2,	8.4 664 4 US-09-904-615-66 Sequence 66, 8.0 2672 1 US-08-703-947-1 Sequence 1,	2 7.9 1342 4 US-09-489-847-89 Sequence 89, 0 7.6 1544 4 US-09-187-999-14 Sequence 14.	9.8 7.5 8920 2 US-08-446-855A-1 Sequence 1,	9.6 7.5 664 4 US-09-904-615-66 Sequence 66,	9.4 7.4 873 3 US-09-475-316A-20 Sequence 20, 8.8 7.3 1378 4 US-09-149-476-208 Sequence 200	8.8 7.3 2323 4 US-09-149-476-24 Sequence 24,	7.3 5232 3 US-08-80-0929A-3 Sequence 3,	8:8 /.3 5232 4 US-US-B1/-US3A-3 Sequence 3, 38 7.2 1582 3 US-08-545-196B-10 Sequence 10,	7.2 1582 3 US-08-545-196B-12 Sequence 12	36 7.1 5656 4 US-09-410-464-5 Sequence 5,	7.6 7.1 732 4 US-09-149-476-66 Sequence 66, 7.1 746 3 US-09-013-810-1 Semience 1.	7.6 7.1 3828 4 US-09-221-013A-7 Sequence 7,	7.1 4344 4 US-09-601-198-165 Sequence 16: 7.1 1664976 4 US-08-916-421B-1 Sequence 1,	7.2 7.0 1492 4 US-09-369-247-23 Sequence 23	37 7.0 1582 3 US-08-545-1968-10 Sequence 10. 37 7.0 1582 3 US-08-545-1968-12 Sequence 12.

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72 TTATTTATTCCCAAATTTTTCTTAAGCAAATATTTCTTTGCTAATCAATAAATTATCAAA 131
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Philadelphia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 9.3%; Score 49.2; DB 1; Length 5852; Best Local Similarity 57.0%; Pred. No. 0.00077; Matches 90; Conservative 0; Mismatches 68; Indels 0
                                                                                                                                                             APPLICANT: Slade, Martin B
APPLICANT: Chang, Andy C M
APPLICANT: Chang, Andy C M
APPLICANT: williams. Keith L
TITLE OF INVENTION: Improved Plasmid Vectors for Cellular
TITLE OF INVENTION: Slime Moulds of the Genus Dictyostelium
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & No. 538952
                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/867,106
PILING DATE: 19920625
PRIOR APPLICATION NUMBER: AU PJ 7187
APPLICATION NUMBER: PCT/AU90/00530
PILING DATE: 02-NOV-1989
ATTONEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             132 AGAAAAAAACTGAAAGCAACGCTTGAAAAAAGGAAA 169
ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: Feeney, Joanne Longo
REGISTRATION NUMBER: 35,134
REFERENCE/DOCKET NUMBER: RICE-0002
TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-568-3100
                                                                                                 Seguence 2, Application US/07867106
Patent No. 5389526
GENERAL INFORMATION:
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INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 5852 base pairs
TYPE: NUCLEIC ACID
STRANDEDNESS: single
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COMPUTER READABLE FORM:
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ANTI-SENSE: NO
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LOCATION:
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US-07-867-106-2
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147 AAGCAACGCTTGAAAAAGGAAAGTTAGCCCTATCGGGTATTTTTGGAAGTTGTA 202
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52.8%; Pred. No. 0.006;
tive 1; Mismatches 82; Indels
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Patent No. 5788962
GENERAL INFORMATION:
APPLICANT: Wise, Kim S.
APPLICANT: McIntosh, Mark A.
TITLE OF INVENTION: DNA Sequences Coding for Mycoplasma
TITLE OF INVENTION: Hyppneumoniae Surface Antigens,
TITLE OF INVENTION: Vaccines and Diagnostic Procedures
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ZIP: 63043
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 5.25 inch, 360 KB storage
COMPUTER: Hewlett-Packard Vectra
OPERATING SYSTEM: MS-DOS Version 3.3
                                                                       TITLE OF INVENTION: 49 Human Secreted Proteins
FILE REPERENCE: P2032P1
FILE REPERENCE: P2032P1
FURENT APPLICATION NUMBER: US/09/904,615
CURRENT FILING DATE: 2001-07-16
FRIOR APPLICATION NUMBER: 09/511,554
FRIOR APPLICATION NUMBER: 60/097,917
FRIOR FILING DATE: 1998-08-25
FRIOR FILING DATE: 1998-08-11
FRIOR FILING DATE: 1998-08-11
NUMBER OF SEQ ID NOS: 170
SOFTWARE: Patentin Ver: 2.0
SOFTWARE: Patentin Ver: 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   n equals a,t,g, or c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME/KEY: SITE
LOCATION: (63)
OTHER INFORMATION: n equals a,t,g, or c
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STREET: 929 Fee Fee Road, Suite 100
             Sequence 66, Application US/09904615
Patent No. 6566325
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Best Local Similarity 52.8
Matches 93; Conservative
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CORRESPONDENCE ADDRESS:
ADDRESSEE: Grace J. 1
                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: SITE
LOCATION: (31)
OTHER INFORMATION: n equ
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Y: USA
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JS-09-904-615-66/c
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1281 TTTTTTTTTTTTTTTTTTTTTTGGAATAATTTTTTTTTAACAGATATAAAA 1222
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                                                                                                                                                                                                                                                                                                                                                                   27 ITTATATGCTGATTTATGGGTGATTTTGCTTCCTTCTTTATACTTTTATTTCCCAAA 86
                                                                                                                                                                                                                                                             40 TTATGGGTGATTTTGCTTCCTTCTTTATACTTTTATTCCCAAATTTTTCCTTAAGCA 99
                                                                                                                                                                                                              Gape
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                                                                                                                                               Score 42.4; DB 1; Length 2672;
Pred. No. 0.04;
0; Mismatches 76; Indels 0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         160 AAAAAGGAAAGTTAGCCCTATCGGGTATATTTTGGAAGTTGTAA 203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        220 AAAAATCAACAAGATTTTTATATTTCTAAATTAAAATTCAAAA 177
                        FILING DATE:
PUBLICATION DATE:
RELEVANT RESIDUES IN SEQ ID NO: From 1 to 2672
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
APPLICANT: Rosen et al
TITLE OF INVENTION: 98 Human Secreted Proteins
FILE REFERENCE: PZ031P1
CURRENT APPLICATION NUMBER: US/09/489, 847
CURRENT FILING DATE: 2000-01-24
CURRENT FILING DATE: 1999-07-29
EARLIER FILING DATE: 1999-07-29
EARLIER FILING DATE: 1998-0-0-6
EARLIER APPLICATION NUMBER: 60/095,486
EARLIER APPLICATION NUMBER: 60/095,486
EARLIER APPLICATION NUMBER: 60/095,486
EARLIER APPLICATION NUMBER: 60/095,486
EARLIER APPLICATION NUMBER: 60/095,454
EARLIER APPLICATION NUMBER: 60/095,454
EARLIER APPLICATION NUMBER: 60/095,455
EARLIER APPLICATION NUMBER: 60/095,455
EARLIER FILING DATE: 1998-08-06
SARLIER FILING DATE: 1998-08-06
NUMBER OF SEQ ID NOS: 376
SOFTWARE: PATENT VOR: 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 89, Application US/09489847
Patent No. 6476195
                                                                                                                                                       8.0%;
                                                                                                                                      Query Match
Best Local Similarity 53.7%
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1161 ACTAAGAG 1154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-489-847-89
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                207 ACTACRIG 214
DOCUMENT NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 4
US-09-489-847-89/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LENGTH: 1342
                                                                                                     US-08-703-947-1
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NAME/KEY: the structural gene for the surface lipoprotein
NAME/KEY: the structural gene for the surface lipoprotein
NAME/KEY: be and includes 312 bp upstream and 479
NAME/KEY: by downstream of coding sequence
LOCATION: coding sequence for P65 spans 1881 bp of
LOCATION: described sequence (begins at nt 313 and
LOCATION includes all sequence through nt 2139)
LOCATION METHOD: by similarity to pattern of open reading
IDENTIFICATION METHOD: frame; by experiment identifying protein products of
IDENTIFICATION METHOD: sequence with immune serum to P65
OTHER INFORMATION: immunogente surface lipoprotein of no known
OTHER INFORMATION: function; C-terminus exposed on external
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ORGANELLE:
IMMEDIATE SOURCE:
LIBRARY: Genomic in Charon 4A, GEM12
LIBRARY: Genomic in Charon 4A, GEM12
CLONE: MhpJ25, MhpJ35, MhpJ35, pZJ25,1, pZJ25.14,
CLONE: pZJG35.1, pZJG35.12, pZJG35.13, pZJG35.14
POSITION IN GENOME:
CHROMOSOME/SEGMENT: single chromosome
MAP POSITION: unknown
UNITS: unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          5.8 kb HindIII fragment from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     hyopneumoniae p65 Surfaée Lipoprotein
Expressed in Escherichia coli from a Cloned
Genomic Fragment
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PUBLICATION INFORMATION:
AUTHORS: Mary F. Kim, Manijeh B. Heidari, Susan J. AUTHORS: Mary F. Kim, Manijeh B. Heidari, Susan J. AUTHORS: Stull, Mark A. McIntosh, and Kim S. Wise TITLE: Identification and Mapping of an TITLE: Immunogenic Region of Mycopleama TITLE: hyopneumoniae p65 Surface Lipoprotein TITLE: hyopneumoniae p65 Surface Lipoprotein TITLE: Appresed in Escherichia coli from a Cloned
             CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/703,947
FILING DATE: 28-AUG-1996
CLASSIFFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/373,957
FILING DATE: January 17, 1995
ATTORNEY/AGENT INFORMATION:
NAME: Fishel, Grace J.
REGISTRATION NUMBER: 25864
REFERENCE/DOCKET NUMBER: 25864
TELECHMUNICATION INFORMATION:
TELECHMUNICATION INFORMATION:
TELECHMUNICATION 1878-0440
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ORGANISM: Mycoplasma hyopneumoniae
STRAIN: J
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TISSUB TYPE:
CELL TYPE: unicellular bacterium
CELL LINE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Infection and Immunity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MOLECULE TYPE: genomic DNA DESCRIPTION: region of 5.8 kd DESCRIPTION: genomic library HYPOTHETICAL: no
                                                                                                                                                                                                                                                                                                                                                                                                            INFORMATION FOR SEQ ID NO: 1: SEQUENCE CHARACTERISTICS: LENGTH: 2672 base pairs TYPE: nucleic acid STRANDEDNESS: single
SOFTWARE: WordPerfect 5.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DEVELOPMENTAL STAGE
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DATE: August 1990
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2637-2643
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FRAGMENT TYPE:
ORIGINAL SOURCE:
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SEQUENCE CHARACTERISTICS:
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                                                                                                                                                       Query Match
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                                       Sequence 14, Application US/09187999A

Patent No. 6482646
GENERAL INFORMATION:
APPLICANT: Gindullis, Frank
APPLICANT: Gindullis, Prank
TITLE OF INVENTION: Plant Proteins that Interact with Nuclear Matrix
TITLE OF INVENTION: Proteins and Function as Transcriptional Activators
FILE REFERENCE: CL-1321
CURRENT APPLICATION NUMBER: US/09/187,999A

CURRENT FILING DATE: 1998-11-06
NUMBER OF SEQ ID NOS: 39
SOFTWARE: Microsoft Office 97
SEQ ID NOS: 39
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Patent No. 5849573

GENERAL INFORMATION:
APPLICANT: Flores, Maria V
APPLICANT: Flores, Maria V
TITLE OF INVENTION: Wholeptide sequence encoding carbamoyl
TITLE OF INVENTION: phosphate synthetase II
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSEE: Nixon & Vanderhye PC
STREET: 1100 No. 5849573th Glebe Road, 8th Floor
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                                                                                                                                                                                                                                                                                                                                                                                                 ch 7.6%; Score 40; DB 4; Length 1544; 1 Similarity 53.1%; Pred. No. 0.14; 85; Conservative 0; Mismatches 75; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    147 AAGCAACGCTTGAAAAAGGAAAGTTAGCCCTATCGGGTA 186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/NS-DOS
SOFTWARE: Patentin Release #1.24
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/446,855A
FILING DATE: 06-Jul-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INPORMATION:
NAME: Mitchard, Leonard C
REGISTRATION NUMBER: 29.009
REFERENCE/DOCKET NUMBER: 47-80
TELECOMMUNICATION INFORMATION:
TELECHONE: 703-816-4100
                                                                                                                                                                                                                                                                                                                                           ; ORGANISM: Lycopersicon esculentum US-09-187-999-14
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INFORMATION FOR SEQ ID NO: 1:
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
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STATE: Virginia
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               RESULT 5
US-09-187-999-14/C
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                                                                                                                                                                                                                                                                                                                         TYPE: DNA
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APPLICANT: Stewart et al.
TITLE OF INVENTION: Nucleotide Sequence Encoding Carbamoyl Phosphate;
PACENT NO. 6183996
TITLE OF INVENTION: Synthetase II
FILE REFERENCE:
CURRENT PAPLICATION NUMBER: US/09/150,741
CURRENT PILLNG DATE: 1998-09-10
EARLIER PILLNG DATE: 1992-12-10
EARLIER PILLNG DATE: 1993-12-02
EARLIER PILLNG DATE: 1993-12-02
EARLIER APPLICATION NUMBER: AU93/00617
EARLIER PILLNG DATE: 1993-12-02
EARLIER APPLICATION NUMBER: 08/446,855
                                                                                                                                                                                                                                                  29 TATATGCTGATTTATGGGTGATTTTGCTTCCTTCTTTATACTTTTATTTCCCAAATT
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                                                                                                                                                        7.5%; Score 39.8; DB 2; Length 8920;
49.7%; Pred. No. 0.35;
tive 1; Mismatches 98; Indels 0
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Pred. No. 0.35;
1; Mismatches 98; Indels 0
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Patent No. 6183996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   209 TACRTGTTCTTTAA 225
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 711 TAAATATAAATGTATAA 727
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; ORGANISM: Plasmodium falciparum
US-09-150-741-1
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LENGTH: 8920 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: genomic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 7.5%;
Best Local Similarity 49.7%;
Matches 98; Conservative
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SOFTWARE: Patentin Ver. 2.0
                                                                                                                                                                                 Best Local Similarity 49.7
Matches 98; Conservative
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APPLICATION NUMBER: 60/047,618
FILING DATE: 1997-05-23
                                                                                                                                                                                                                                                                                                                                                                              85; Conservative
                                                                                                                                                                TYPE: DNA
ORGANISM: Thuja plicata
                                                                                                                                                                                                                                  ) NAME/KEY: CDS
; LOCATION: (25)..(591)
US-09-475-316A-20
                                                                                                                                                                                                                                                                                                                                                 Best_Local Similarity
Matches 85; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-09-149-476-208/c
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                                                                                                                                                                                                                 FEATURE:
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APPLICANT: Lewis, No. 6210942man G.
APPLICANT: Davin, Laurence B.
APPLICANT: Davin, Laurence B.
APPLICANT: Davin, Laurence B.
APPLICANT: Davin, Laurence B.
APPLICANT: Fujita, Masayuki
APPLICANT: Gang, David R.
APPLICANT: Gang, David R.
APPLICANT: Gang, David R.
APPLICANT: Sarkanen, Simo
APPLICANT: Pord, Joshua D
TITLE OF INVENTION: RECOMBINANT PINORESINOL/LARICIRESINOL REDUCTASES,
TITLE OF INVENTION: RECOMBINANT DIRIGENT PROTEINS AND METHODS OF USE
FILE REFERENCE: WSUR-1-13793
CURRENT FILING DATE: 1999-12-30
PRIOR APPLICATION NUMBER: 09/307,653
PRIOR FILING DATE: 1999-12-07
PRIOR FILING DATE: 1997-11.07
PRIOR FILING DATE: 1997-11.07
PRIOR FILING DATE: 1997-11.07
PRIOR PULICATION NUMBER: 60/054,380
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            26 ATTIATATGCTGATTTATGGGTGATTTTGCTTCCTTCTTTATACTTTTATTTTATTCCCAA
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                                                                                                                                                                            TITLE OF INVENTION: 49 Human Secreted Proteins
FILE REPERRNCE: PZ032P1
CURRENT APPLICATION NUMBER: US/09/904,615
CURRENT FILING DATE: 2000-07-16
PRIOR APPLICATION NUMBER: 09/511,554
PRIOR APPLICATION NUMBER: 60/097,917
PRIOR APPLICATION NUMBER: 60/097,917
PRIOR PILING DATE: 1998-08-25
PRIOR PILING DATE: 1998-08-25
PRIOR PILING DATE: 1998-08-11
NUMBER OF SEQ ID NOS: 170
SOFTWARE: Patentin Ver: 2.0
SOFTWARE: Patentin Ver: 2.0
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LOCATION: (63)
SOTHER PROBRATION: n equals a,t,g, or C
US-09-904-615-66
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US-09-475-316A-20/c
Sequence 20, Application US/09475316A
; Patent No. 6210942
                                                                                           US-09-904-615-66
; Sequence 66, Application US/09904615
; Patent No. 6566325
; GENERAL INFORMATION:
711 TAAATATAAATGTATAA 727
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Best Local Similarity 54.24
Matches 78; Conservative
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LOCATION: (31)
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913 TAAACAGCCAAATACATTATTCTCAACTTACAAGACTCTCCAAATACTTAACAATTATC 754
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| Sequence 208, Application US/09149476
| Patent No. 6420526
| GENERAL INPORMATION:
| APPLICANT: Rosen et al. |
| TITLE OF INVENTION: 186 Human Secreted proteins |
| TITLE OF INVENTION: 186 Human Secreted proteins |
| TITLE OF INVENTION: 186 Human Secreted proteins |
| CURRENT FILING DATE: 1998-09-08 |
| EARLIER APPLICATION NUMBER: US/09/149,476 |
| EARLIER PILING DATE: 1998-03-06 |
| EARLIER PILING DATE: 1997-03-07 |
| EARLIER APPLICATION NUMBER: 60/040,162 |
| EARLIER FILING DATE: 1997-03-07 |
| EARLIER FILING DATE: 1997-03-07 |
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R APPLICATION NUMBER: 60/047,600
R FILING DATE: 1997-05-23
R APPLICATION NUMBER: 60/047,615
R FILING DATE: 1997-05-23
R APPLICATION NUMBER: 60/047,597
R FILING DATE: 1997-05-23
R APPLICATION NUMBER: 60/047,502
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APPLICATION NUMBER: 60/047,633
FILING DATE: 1997-05-23
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PRIOR FILING DATE: 1997-07-31
PRIOR APPLICATION VUMBER: 60/030,522
PRIOR FILING DATE: 1996-11-08
NUMBER OF SEQ ID NOS: 122
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO.
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FILING DATE: 1997-08-22

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BARLIER FILING DATE: 1997-05-23
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R FILING DATE: 1997-08-22

R APPLICATION NUMBER: 60/056,879

R FILING DATE: 1997-08-22

R APPLICATION NUMBER: 60/056,880

R FILING DATE: 1997-08-22

R APPLICATION NUMBER: 60/056,991

R FILING DATE: 1997-08-22

R APPLICATION NUMBER: 60/056,911

R FILING DATE: 1997-08-22

R APPLICATION NUMBER: 60/056,836

R FILING DATE: 1997-08-22

R APPLICATION NUMBER: 60/056,814

R FILING DATE: 1997-08-22

R APPLICATION NUMBER: 60/056,814

R FILING DATE: 1997-08-22

R APPLICATION NUMBER: 60/056,910

R FILING DATE: 1997-08-22

R APPLICATION NUMBER: 60/056,910

R FILING DATE: 1997-08-22

R APPLICATION NUMBER: 60/056,910

R FILING DATE: 1997-08-22

R APPLICATION NUMBER: 60/056,912

R FILING DATE: 1997-08-22

R APPLICATION NUMBER: 60/056,913

R FILING DATE: 1997-08-22

R APPLICATION NUMBER: 60/056,915

R FILING DATE: 1997-08-22

R APPLICATION NUMBER: 60/056,915

R FILING DATE: 1997-08-22 R FILING DATE: 1997-08-22
R APPLICATION NUMBER: 60/057,761
R FILING DATE: 1997-08-22
R APPLICATION NUMBER: 60/047,595
R FILING DATE: 1997-05-23
R APPLICATION NUMBER: 60/047,599 R FILING DATE: 1997-05-23

R APPLICATION NUMBER: 60/047,594

R FILING DATE: 1997-05-23

R PILING DATE: 1997-05-23

R FILING DATE: 1997-05-23

R APPLICATION NUMBER: 60/047,599 A APPLICATION NUMBER: 60/043,670
R FILING DATE: 1997-04-11
R APPLICATION NUMBER: 60/056,632
R APPLICATION NUMBER: 60/056,664
R APPLICATION NUMBER: 60/056,664 FILING DATE: 1997-05-23
APPLICATION NUMBER: 60/047,588
FILING DATE: 1997-05-23
APPLICATION NUMBER: 60/047,585
FILING DATE: 1997-05-23 FILING DATE: 1997-05-23
APPLICATION NUMBER: 60/047,614
FILING DATE: 1997-05-23
APPLICATION NUMBER: 60/043,578
FILING DATE: 1997-04-11 APPLICATION NUMBER: 60/056,903 FILING DATE: 1997-08-22 APPLICATION NUMBER: 60/056,888 APPLICATION NUMBER: 60/047,586 FILING DATE: 1997-05-23 APPLICATION NUMBER: 60/047,590 APPLICATION NUMBER: 60/043,576 FILING DATE: 1997-04-11 APPLICATION NUMBER: 60/047,501 APPLICATION NUMBER: 60/056,909 FILING DATE: 1997-08-22 APPLICATION NUMBER: 60/056,875 APPLICATION NUMBER: 60/056,862 FILING DATE: 1997-08-22 APPLICATION NUMBER: 60/056,887 FILING DATE: 1997-08-22 APPLICATION NUMBER: 60/056,876 FILING DATE: 1997-08-22 APPLICATION NUMBER: 60/056,881 FILING DATE: 1997-05-23 FILING DATE: 1997-08-2 BARLIER
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R APPLICATION NUMBER: 60/047, 581

R FILING DATE: 1997-05-23

R PILING DATE: 1997-05-23

R PILING DATE: 1997-05-23

R APPLICATION NUMBER: 60/047, 584

R APPLICATION NUMBER: 60/047, 580

R PILING DATE: 1997-05-23

R APPLICATION NUMBER: 60/047, 492

R APPLICATION NUMBER: 60/047, 492

R APPLICATION NUMBER: 60/047, 598

R APPLICATION NUMBER: 60/047, 598

R APPLICATION NUMBER: 60/047, 598

R APPLICATION NUMBER: 60/047, 598

R PILING DATE: 1997-05-23

R APPLICATION NUMBER: 60/047, 598

R PILING DATE: 1997-05-23

R APPLICATION NUMBER: 60/047, 598

R PILING DATE: 1997-05-23

R APPLICATION NUMBER: 60/047, 592

R PRILING DATE: 1997-05-23
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R APPLICATION NUMBER: 60/043,314

R PLING DATE: 1997-04-11

R APPLICATION NUMBER: 60/043,569

R FILING DATE: 1997-04-11

R APPLICATION NUMBER: 60/043,311

R APPLICATION NUMBER: 60/043,671

R APPLICATION NUMBER: 60/043,674

R PILING DATE: 1997-04-11

R PELLING DATE: 1997-04-11

R PELLING DATE: 1997-04-11

R PELLING DATE: 1997-04-11
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REPLICATION NUMBER: 60/043,312
REFLICATION NUMBER: 60/043,313
REFLICATION NUMBER: 60/043,313
REFLICATION NUMBER: 60/043,672
REPLICATION NUMBER: 60/043,672
REPLICATION NUMBER: 60/043,315
REPLICATION NUMBER: 60/048,315
REPLICATION NUMBER: 60/048,974
REFLICATION NUMBER: 60/048,974
REFLICATION NUMBER: 60/056,886
REPLICATION NUMBER: 60/056,886
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R APPLICATION NUMBER: 60/047,632

R FILING DATE: 1997-05-23

R APPLICATION NUMBER: 60/047,601

R FILING DATE: 1997-05-23

R APPLICATION NUMBER: 60/043,580
                                                                                                                                           FILING DATE: 1997-05-23
APPLICATION NUMBER: 60/047,503
FILING DATE: 1997-05-23
APPLICATION NUMBER: 60/047,592
FILING DATE: 1997-05-23
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APPLICATION NUMBER: 60/047,612
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APPLICATION NUMBER: 60/043,568
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1293 ACTCTGATAAATTTATTAAAATAAGAACAAGCATCAGTTGTACATAGAAATAATCATTTG 1234
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         147 AAGCAACGCTTGAAAAAGGAAAGTTAGCCCTATCGGGTATATTTTGGAAGTTGTAAAAT 206
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TTTATATGCTGATTTATGGGTGATTTTGCTTCCTTCTTTATACTTTTATTTTTCCCAAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     7.3%; Score 38.8; DB 4; Length 1378; 47.8%; Pred. No. 0.29; tive 1; Mismatches 118; Indels 0
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CURRENT FILING DATE: 1998-09-08
EARLIER APPLICATION NUMBER: US/09/149,476
CURRENT FILING DATE: 1998-03-06
EARLIER FILING DATE: 1997-03-07
EARLIER FILING DATE: 1997-03-07
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                             EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/048,964
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EARLIER FILING DATE: 1997-06-06
EARLIER FILING DATE: 1997-09-05
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APPLICATION NUMBER: 60/047,583
APPLICATION NUMBER: 60/056,908
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Patent No. 6420526
GENERAL INFORMATION:
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Matches 109; Conservative
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FILING DATE: 1997-08-22
APPLICATION NUMBER: 60/056,880
FILING DATE: 1997-08-22
APPLICATION NUMBER: 60/056,894
FILING DATE: 1997-08-22
APPLICATION NUMBER: 60/056,911
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G DATE: 1997-05-23
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DATE: 1997-05-23
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4G DATE: 1997-05-23
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DATE: 1997-05-23
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PLICATION NUMBER: 60/043,576
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PLICATION NUMBER: 60/056,876
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FILING DATE: 1997-08-22
APPLICATION NUMBER: 60/056,875
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PLICATION NUMBER: 60/056,882
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LING DATE: 1997-08-22
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PLICATION NUMBER: 60/056,631
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LING DATE: 1997-05-23
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ING DATE: 1997-05-23
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LING DATE: 1997-08-22
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ING DATE: 1997-08-22
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ATION NUMBER: 60/056,864
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APPLICANT: Korneluk, Robert G
APPLICANT: MacKenzie, Alexander E
APPLICANT: MacKenzie, Alexander E
APPLICANT: MacKenzie, Alexander E
APPLICANT: Listen, Peter
APPLICANT: Tang, Baird, Stephen
APPLICANT: Trang, Benjamin K
APPLICANT: Trang, Benjamin K
APPLICANT: Trang, Benjamin K
TITLE OF INVENTION: DISEASE
TITLE OF INVENTION: DISEASE
TITLE OF INVENTION: DISEASE
TITLE OF INVENTION: DISEASE
FILE REFERENCE: 07891/009002
CURRENT APPLICATION NUMBER: US/09/212, 971B
CURRENT APPLICATION NUMBER: 60/017,354
EARLIER PILING DATE: 1996-04-26
EARLIER PILING DATE: 1996-11-14
EARLIER PILING DATE: 1996-11-14
EARLIER PILING DATE: 1996-11-14
EARLIER PILING DATE: 1997-02-13
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Pred. No. 0.36;
1; Mismatches 118; Indels 0
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SOFWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 3
LENGTH: 5232
                                                                           RR FILING DATE: 1997-08-22
RR APPLICATION NUMBER: 60/056,908
RR FILING DATE: 1997-08-22
RR APPLICATION NUMBER: 60/048,964
RR FILING DATE: 1997-06-06
RR APPLICATION NUMBER: 60/057,650
RR RILING DATE: 1997-09-05
RR FILING DATE: 1997-09-05
RR APPLICATION NUMBER: 60/056,884
RR FILING DATE: 1997-08-22
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APPLICATION NUMBER: 60/061,060
FILING DATE: 1997-10-02
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FILING DATE: 1997-09-05
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                                      1997-08-22
1997-08-22
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                                      FILING DATE: 1997-08
APPLICATION NUMBER:
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ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: variation
LOCATION: (4623)...(4623)
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Best Local Similarity 47.8<sup>1</sup>
Matches 109; Conservative
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APPLICANT: MacKenzie, Alexander E
APPLICANT: MacKenzie, Alexander E
APPLICANT: Liston, Peter
APPLICANT: Liston, Peter
APPLICANT: Baird, Stephen
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US-08-545-196B-10/c
Sequence 10, Application US/08545196B
Fatent No. 6080577
GENERAL INFORMATION:
APPLICANT: MELKI, JUDITH
APPLICANT: MUNNICH, ARNOLD
TITLE OF INVENTION: SURVIVAL MOTOR NEURON (SMN) GENE: A GENE
TITLE OF INVENTION: FOR SPINAL MUSCULAR ATROPHY
                                                                                                                                             Score 38.8; DB 3; Length 5232;
Pred. No. 0.52;
0; Mismatches 37; Indele 0
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Pred. No. 0.52;
0; Mismatches 37; Indels 0
   ; LOCATION: 1...5232
; OTHER INFORMATION: N at 4622 and 4633 can be A, G, T or US-08-800-929A-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2394 raagrargrarracrirrgraarcagaarrrrragaaa 2431
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CTHER INFORMATION: n can be any nucleotide
NAME/KRY: variation
LOCATION: (4622) ... (4622)
COTHER INFORMATION: n can be any nucleotide
US-09-617-053A-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 3, Application US/09617053A Patent No. 6300492
                                                                                                                                                 Query Match 7.3%;
Best Local Similarity 62.2%;
Matches 61; Conservative
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Best Local Similarity 62.2%;
Matches 61; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME/KEY: variation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 14
US-09-617-053A-3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   34 GCTGATTTATGGGTGATTTTGCTTCCTTTTATACTTTTATTTTTATTCCCAAATTTTTCT 93
                                                                                                                                                                                                                                                                                                                                Gaps
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                                                                                                                                                                                                                                                  Score 38.8; DB 3; Length 5232;
Pred. No. 0.52;
0; Mismatches 37; Indels 0
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ZUDIATIO 1 USA
ZUDIATIO 2110
COMPUTER READABLE FORM:
MEDLUM TYPE: DasAction
COPERATING SYSTEM: DOS
SOFTWARE: PASISEO COFT WINDOWS VERSION 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/800,929A
CLASSIFICATION DATA:
APPLICATION NUMBER: 60/030,590
FILING DATE: 14-NOV-1996
APPLICATION NUMBER: 60/017,354
FILING DATE: 14-NOV-1996
ATTORNEY, AGENT INFORMATION:
NAME: BLOKEY-BREAD, Kristina
REGISTRATION NUMBER:
                                                               NAME/KEY: variation
CCATION: (4622)
DCATION: (4622)
OTHER OF A OTHER OTHER OTHER OTHER OTHER OTHER OTHER OTHER OTHER OTHER OTHER OTHER OTHER OTHER OTHER OTHER OTHER OTHER OTHER OTHER OTHER OTHER OTHER OTHER OTHER OTHER O
OTHER INFORMATION: n can be any nucleotide
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-428-0200
TELEFAX: 617-428-7045
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Korneluk, Robert G
APPLICANT: MacKenzie, Alexander E
APPLICANT: Liston, Peter
APPLICANT: Baird, Stephen
APPLICANT: Tanng, Benjamin K
APPLICANT: Pratt, Christine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 3, Application US/08800929A Patent No. 6133437 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     E: Clark & Elbing LLP
176 Federal Street
                                                                                                                                                                                                                                              Query Match
Best Local Similarity 62.2%;
Matches 61; Conservative (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS: LENGTH: 5232 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CORRESPONDENCE ADDRESS:
ADDRESSEE: Clark & E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MOLECULE TYPE: CDNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COUNTRY:
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GENERAL INFORMATION:
APPLICANT: SHAO, Wei et al
TITLE OF INVENTION: ISOLATED HUMAN ENZYME PROTEINS, NUCLEIC
TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN ENZYME PROTEINS, AND USES
TITLE OF INVENTION: THEREOF
TITLE OF INVENTION: THEREOF
CURRENT PAPLICANING
CURRENT FAILING DAITE: 2001-03-29
NUMBER OF SEQ ID NOS: 4
SOFTWARE: PASLESEQ for Windows Version 4.0
SEQ ID NO 3
LENGTH: 18853
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               25 GATTTATATGCTGATTTATGGCTGATTTTGCTTCCTTCTTTATACTTTTATTATTCCCA
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Pred. No. 0.51;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    90; Indels
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                    OPERATION SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/545,196B
FILING DATE: 19-OCT-1995
CLASSIFICATION: 435
ATORNEY/AGENT INFORMATION:
NAME: PRARACI, C. J.
REGISTRATION NUMBER: 32,350
REGISTRATION NUMBER: 32,350
REGISTRATION NUMBER: 2121-110P
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 205-8050
INFORMATION FOR SEQ 1D NO: 12:
SEQUENCE CHARACTERISTICS:
LEMETHER CHARACTERISTICS:
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Best Local Similarity 50.5%; Pred. No. 1.5;
Matches 92; Conservative 0; Mismatches
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US-07HER INFORMATION: n = A,T,C or G
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Best Local Similarity 50.5%;
Matches 92; Conservative (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: CDNA
US-08-545-1968-12
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| AC 1377
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ORGANISM: Human
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US-09-820-005-3/c
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APPLICANT: MELKI, JUDITH
APPLICANT: MELKI, JUDITH
APPLICANT: MUNICH, ARNOLD
TITLE OF INVENTION: SURVIVAL MOTOR NEURON (SMN) GENE: A GENE
TITLE OF INVENTION: FOR SPINAL MUSCULAR ATROPHY
NUMBER OF SEQUENCES: 65
CORRESPONDENCE ADDRESS:
ADDRESSEE: BIRCH, STEWART, KOLASCH AND BIRCH, LLP
STREET: PO BOX 747
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 3; Length 1582,
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                                                                                                                                                                  COUNTRY: USA

COUNTRY: USA

ZIP: 22040-0747

COMPUTER READABLE FORM:
MEDIUM TYPE: Ploppy disk
COMPUTER: IBM PC Compatible
COMPUTER: Patentin Release #1.0, Version #1.30

SOFTWARE: Patentin Release #1.0, Version #1.30

CURENT APPLICATION DATA:
APPLICATION NUMBER: US/08/545,196B

FILING DATE: 19-0CT-1995
CLASSIFICATION: 435
ATTORNEY/ABENT INFORMATION:
NAME: FARACI, C. J.
REGISTRATION NUMBER: 32,350

REFERENCE/DOCKEY NUMBER: 2121-110P
TELECOMMUNICATION INFORMATION:
TELECHONE: (703) 205-8000
TELECHONE: (703) 205-8000
TELEFAX: (703) 205-8000
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
**TOWATH: 1582 base pairs
                                                         ADDRESSEE: BIRCH, STEWART, KOLASCH AND BIRCH, LLP
STREET: PO BOX 747
CITY: FALLS CHURCH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEE: BIRCH, STEWART, KOLASCH AND BIRCH, LLP: PO BOX 747
FALLS CHURCH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 38; DB 3;
Pred. No. 0.51;
0; Mismatches
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US-08-545-196B-12/c
; Sequence 12, Application US/08545196B
; Patent No. 6080577
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 7.2%;
Best Local Similarity 50.5%;
Matches 92; Conservative
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LENGTH: 1582 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
NUMBER OF SEQUENCES: 65
                              CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MOLECULE TYPE: CDNA
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STATE: V?
COUNTRY:
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R FILING DATE: 1997-03-07
R APPLICATION NUMBER: 60/047,600
R PILING DATE: 1997-05-23
R RILING DATE: 1997-05-23
R RILING DATE: 1997-05-23
R REPLICATION NUMBER: 60/047,597
R FILING DATE: 1997-05-23
R RAPLICATION NUMBER: 60/047,502
                                                                                                                                                                                                                                                                                                                                                                R FILING DATE: 1997-05-23

R APPLICATION NUMBER: 60/047,583

R PILING DATE: 1997-05-23

R APPLICATION NUMBER: 60/047,617

R APPLICATION NUMBER: 60/047,618

R APPLICATION NUMBER: 60/047,503

R APPLICATION NUMBER: 60/047,503

R APPLICATION NUMBER: 60/047,503
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FILING DATE: 1997-05-23
APPLICATION NUMBER: 60/047,581
ELING DATE: 1997-05-23
APPLICATION NUMBER: 60/047,584
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE: 1997-05-23
APPLICATION NUMBER: 60/047,601
FILING DATE: 1997-05-23
APPLICATION NUMBER: 60/043,580
FILING DATE: 1997-04-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: 60/043,568
FILING DATE: 1997-04-11
APPLICATION NUMBER: 60/043,314
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FILING DATE: 1997-04-11
APPLICATION NUMBER: 60/043,311
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APPLICATION NUMBER: 60/043,315
FILING DATE: 1997-04-11
                                                           'ILING DATE: 1997-03-07
APPLICATION NUMBER: 60/040,163
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APPLICATION NUMBER: 60/047,500
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APPLICATION NUMBER: 60/047,492
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APPLICATION NUMBER: 60/047,598
FILING DATE: 1997-05-23
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APPLICATION NUMBER: 60/047,582
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APPLICATION NUMBER: 60/043,669
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APPLICATION NUMBER: 60/043,312
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APPLICATION NUMBER: 60/043,313
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                                                                                                                                                                                                                                                                                                                  FILING DATE: 1997-05-23
APPLICATION NUMBER: 60/047,633
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APPLICATION NUMBER: 60/047,587
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APPLICATION NUMBER: 60/047,632
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FILING DATE: 1997-04-11
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15117 GGTTTGTTTTTTTTTTTTTTTTCAGTAIGAAATCCATCTGTTCCAGCAC 15058
                                                                                                                14997 AAAAGAAAACTTTGCATAATACAAGGTTCACATAAAACCCAATTCTTGGCTGGTGGGGG 14938
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           60 TICTITATACTITIATITATICCCAAATTITICTIAAGCAAATATITCTITGCTAATCAA 119
                                                                                APPLICANT: Strauss et al.

TITLE OF INVENTION: Floral homeotic genes for manipulation of flowering in TITLE OF INVENTION: poplar and other plant species.

TITLE OF INVENTION: poplar and other plant species.

FILE REFERENCE: 53375

CURRENT PELICANION NUMBER: US/09/410,464

EARLIER FILING DATE: 1999-10-01

EARLIER FILING DATE: 1999-04-06

EARLIER FILING DATE: 1999-04-06

EARLIER FILING DATE: 1998-04-06

SARLIER FILING DATE: 1998-04-06

SOFTWARE: PARENCE: 2.0

SEQ ID NO 5: 24

SEQ ID NO 5: 24
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              120 TAAATTATCAAAAGAAAAAAAACTGAAAGCAACGCTTGAAAAAAGGAAAGTT 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TITLE OF INVENTION: 186 Human Secreted proteins
TITLE OP INVENTION: 186 Human Secreted proteins
FILE REPERENCE: P2002P1
CURRENT APPLICATION NUMBER: US/09/149,476
CURRENT FILING DATE: 1998-09-08
EARLIER APPLICATION NUMBER: PCT/US98/04493
EARLIER PILING DATE: 1997-03-07
EARLIER PILING DATE: 1997-03-07
EARLIER FILING DATE: 1997-03-07
EARLIER FILING DATE: 1997-03-07
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EARLIER FILING DATE: 1997-03-07
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; TYPE: DNA
; ORGANISM: Populus balsamifera subsp. trichocarpa
US-09-410-464-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 19
US-09-149-476-66
; Sequence 66, Application US/09149476
; Batent No. 6420526
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 5, Application US/09410464
Patent No. 6395892
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FILING DATE: 1997-04-11

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RAKLIER APPLICATION UNDERS: 60/95, 896

RAKLIER PELILING DATE: 1997-06-02

EARLIER FILING DATE: 1997-06-02

EARLIER FILING DATE: 1997-06-02

EARLIER FILING DATE: 1997-06-02

EARLIER FILING DATE: 1997-06-02

EARLIER APPLICATION NUMBER: 60/056, 893

EARLIER FILING DATE: 1997-06-22

EARLIER APPLICATION NUMBER: 60/056, 893

EARLIER APPLICATION NUMBER: 60/056, 893

EARLIER APPLICATION NUMBER: 60/056, 893

EARLIER APPLICATION NUMBER: 60/056, 893

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EARLIER APPLICATION NUMBER: 60/056, 893

EARLIER APPLICATION NUMBER: 60/056, 893

EARLIER APPLICATION NUMBER: 60/056, 893

EARLIER FILING DATE: 1997-08-22

EARLIER FILING DATE: 1997-08-22

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EARLIER FILING DATE: 1997-08-22

EARLIER FILING DATE: 1997-08-22

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EARLIER FILING DATE: 1997-08-22

EARLIER FILING DATE: 1997-08-22

EARLIER PAPLICATION NUMBER: 60/056, 915

EARLIER PAPLICATION NUMBER: 60/056, 915

EARLIER PAPLICATION NUMBER: 60/056, 915

EARLIER APPLICATION NUMBER: 60/056, 915

EARLIER APPLICATION NUMBER: 60/056, 915

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EARLIER APPLICATION NUMBER: 60/056, 915

EARLIER APPLICATION NUMBER: 60/056, 915

EARLIER APPLICATION NUMBER: 60/047, 595

EARLIER FILING DATE: 1997-08-22

EARLIER FILING DATE: 1997-08-22

EARLIER FILING DATE: 1997-08-22

EARLIER FILING DATE: 1997-08-22

EARLIER FILING DATE: 1997-08-22

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EARLIER FILING DATE: 1997-08-22

EARLIER FILING DATE: 1997-08-22

EARLIER FILING DATE: 1997-08-22

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Sequence 1, Application US/09013810

Patent No. 6197551

GENERAL INFORMATION:

TITLE OF INVENTION: No. 6197551el TANGO 80 Molecules and Uses Thereof

TITLE OF INVENTION: No. 6197551el TANGO 80 Molecules and Uses Thereof

NUMBER OF SEQUENCES:

ADDRESSEE: LAHIVE & COCKFIELD, LLP

STREET: 28 State Street

CITY: Boston

STATE: Massachusetts

CONTRY: USA

ZIP: 02109

COMPUTER: REDABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM FC Compatible

COMPUTER: IBM FC Compatible

COMPUTER: TBM FC Compatible

SOFTWARE: PatentIn Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             46 GTGATTTTGCTTCCTTTTATACTTTTATTTTCCCCAAATTTTTCTTAAGCAAATATT 105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         106 TCTTTGCTAATCAATAAATTATCAAAAGAAAAAAAAAACTGAAAGCAACGCTTGAAAAAG 165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       604 Grcagriricgaarcricgaaagririaargririrarraggagarriaaagaaaraaa 663
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                                                              ER FILING DATE: 1997-04-11

ER PLING DATE: 1997-04-11

ER APPLICATION NUMBER: 60/056,632

ER APPLICATION NUMBER: 60/056,664

ER FILING DATE: 1997-08-22

ER PILING DATE: 1997-08-22

ER PLING DATE: 1997-08-22

ER APPLICATION NUMBER: 60/056,891

ER FILING DATE: 1997-08-22

ER APPLICATION NUMBER: 60/056,895

ER FILING DATE: 1997-08-22

ER PILING DATE: 1997-08-22

ER PILING DATE: 1997-08-22

ER PELING DATE: 1997-08-22

ER APPLICATION NUMBER: 60/056,805

ER PELING DATE: 1997-08-22

ER APPLICATION NUMBER: 60/056,862

ER PELING DATE: 1997-08-22

ER APPLICATION NUMBER: 60/056,862

ER PELING DATE: 1997-08-22

ER PELING DATE: 1997-08-22
APPLICATION NUMBER: 60/047,501
FILING DATE: 1997-05-23
APPLICATION NUMBER: 60/043,670
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE: 1997-08-22
APPLICATION NUMBER: 60/048,964
FILING DATE: 1997-06-06
APPLICATION NUMBER: 60/057,650
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FILING DATE: 1997-08-22
APPLICATION NUMBER: 60/057,669
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FILING DATE: 1997-06-13
APPLICATION NUMBER: 60/061,060
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EARLIER FILING DATE: 1997-10-02
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Matches 70; Conservative
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US-08-916-421B-1
      Matches
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APPLICANT: Williamson, Richard E.
APPLICANT: Williamson, Richard E.
APPLICANT: Berzner, Andreas S.
APPLICANT: Berzner, Andreas S.
APPLICANT: Berzner, Andreas S.
TITLE OF INVENTION: Manipulation of cellulose and/or Beta-1,4-glucan FILE OF INVENTION: Manipulation of cellulose and/or Beta-1,4-glucan FILE DETERMINE: 96-98
FILE OF BELING DATE: 1991-23
PRIOR APPLICATION NUMBER: PCT/AU97/00402
PRIOR APPLICATION NUMBER: PCT/AU97/00402
PRIOR APPLICATION NUMBER: 1996-6-27
PRIOR FILING DATE: 1996-6-27
PRIOR FILING DATE: 1996-6-27
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ouery Match 7.1%; Score 37.6; DB 3; Length 746; Best Local Similarity 54.3%; Pred. No. 0.47; Matches 76; Conservative 0; Mismatches 64; Indels
                                                  CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME:
ATTORNEY/AGENT INFORMATION:
REGISTRATION NUMBER: 36,207
REGISTRATION NUMBER: 36,207
REGISTRATION NUMBER: MEI-010
RELEPHONE: (617)22-7400
TELECHONEN: (617)742-4214
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 746 base pairs
TYRE: nucleic acid
STRANBENNESS: single
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/013,810
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 7, Application US/09221013A
Patent No. 6495740
GENERAL INFORMATION:
APPLICANT: Arioli, Antonio
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      147 AAGCAACGCTTGAAAAAGG 166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              611 ATGCTTTGGATGAAACATG 592
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: DNA ORGANISM: Arabidopsis thaliana
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Patentin Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; NAME/KEY: CDS
; LOCATION: (239)..(3490)
US-09-221-013A-7
                                                                                                                                                                                                                                                                                                                                                                                                                                      ; NAME/KEY: CDS
; LOCATION: 135..428
US-09-013-810-1
                                                                                                                                                                                                                                                                                                                                                                                  TOPOLOGY: linear MOLECULE TYPE: CDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
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SEQ ID NO 7
LENGTH: 3828
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US-09-221-013A-7
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GENERAL INFORMATION:
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APPLICANT: Bult et al.
TITLE OF INVENTION: Complete Genome Sequence of the Methanogenic Archaeon, Methanococc
Patent No. 6503729
TITLE OF INVENTION: jannaschii
FILE REPERENCE: 18275
CURRENT APPLICATION NUMBER: US/08/916,421B
CURRENT FILING DATE: 1997-08-22
FRIOR FILING DATE: 1996-08-22
NUMBER OF SEQ ID NOS: 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SQUENCE 165, Application US/09601198

| SAGUENCE 165, Application US/09601198
| Patent No. 6511583
| GENERAL INFORMATION:
| APPLICANT: Casell, Gail H.
| APPLICANT: Glass, John I.
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                                                                                                                                                                                               3671 ATTGTTTGTTTTTTTTTTTTGTACTTTTTAGTTATTCCGTAGTTATTGTATAGT 3730
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                                                                                                       42 ATGGGTGATTTTGCTTCCTTCTTTATACTTTTATTTTCCCAAATTTTTCTTAAGCAAA 101
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                                                                                                                                                                                                                                                                                                 102 TATTTCTTTGCTAATGAATTATCAAAAGAAAAAAAGTGAAAGCAACGCTTGAAA
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0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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Pred. No. 1;
0; Mismatches 64; Indels 0;
     54; Indels
          0; Mismatches
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Patent No. 6503729
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   148 AGCAACGCTTGAAAAAGGA 167
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ORGANISM: Ureaplasma urealyticum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 7.1%;
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Best Local Similarity 54.3
Matches 76; Conservative
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SOFTWARE: Patentin version 3.1 SEQ ID NO 1 LENGTH: 1664976 TYPE: DNA	: Methanococcus J : Misc feature : (28222)(28222	KEY: misc feature ION: (28257)(28258)	RMATION: n equals misc feature (84773) (84773)		(848 <u>0</u> ORMATI	NAME/KEY: MISC feature LOCATION: (84812)(84812) OTHER INFORMATION: n equals	(98120). (98120) (98NATION: n equals	: misc_reacure : (98159)(98159) FORMATION: n equals	: misc_feature : (98239)(98239) FORMATION: n equals	KEY: misc feature ION: (98266)(98266)	misc_feature	FORMATION: n equals	misc_reacure (103998)(103998)	information: n equals KEY: misc_feature	LOCATION: (148948) . (148948) OTHER INFORMATION: n equals	NAME/KEY: misc_feature LOCATION: (163385)(163385)	KEY: misc featu	n equals	LOCATION: (191995)(191995) OTHER INFORMATION: n equals	NAME/KEY: misc_feature LOCATION: (231980)(231980) OTHER INFORMATION: n equals	KBY: misc feature ION: (234187)(23418	misc feature	(234220) (234220) NRMATION: n equals	LOCATION: MISC reacure LOCATION: (234814) (234ER INFORMATION: n equals	KBY: misc_feature ION: (309398)(30939	n equals ure	(309418)(309418) RMATION: n equals	misc_feature_ (312837)(312837) ORMATION: n equals	Ę

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OTHER INFORMATION: n equals a, to LOCATION: (319226)...(319226)

OTHER INFORMATION: n equals a, to NAME/KEY: misc\_feature LOCATION: (559167)...(559167)

OTHER INFORMATION: n equals a, to NAME/KEY: misc\_feature LOCATION: (559241)...(559241)

OTHER INFORMATION: n equals a, to NAME/KEY: misc\_feature LOCATION: (650992)...(600992)

OTHER INFORMATION: n equals a, to NAME/KEY: misc\_feature LOCATION: (657081)...(173652)...(773676)...(7 NAME/KEY: misc feature
LOCATION: (1349473)...(1349473)
OTHER INFORMATION: n equals a, t,
NAME/KEY: misc feature
LOCATION: (134991)...(1349491)
OTHER INFORMATION: n equals a, t,
NAME/KEY: misc feature
LOCATION: (1470091)...(1470091)

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87 ITITICITAAGCAAATAITICITIGCIAATCAATAAATTATCAAAAGAAAAAAAAACTGA 146
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STREET: One Liberty Place 46th Ploor
CITY: Philadelphia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ch 7.0%; Score 37.2; DB 1; Length 5852; 1 Similarity 56.6%; Pred. No. 1.5; 69; Conservative 0; Mismatches 53; Indels 0
                                                                                               Sequence 2, Application US/07867106
Patent No. 5389526
GENERAL INFORMATION:
APPLICANT: Slade, Martin B
APPLICANT: Chang, Andy C M
APPLICANT: Chang, Man Keith L
TITLE OF INVENTION: Improved Plasmid Vectors for Cellular
TITLE OF INVENTION: 11me Moulds of the Genus Dictyostellum
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
ADDRESSER: Woodcock Washburn Kurtz Mackiewicz & No. 5189679
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CURRENT APPLICATION DATA:

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/07/867,106

FILING DATE: 19920625

PRIOR APPLICATION DATA:

APPLICATION NUMBER: AU PJ 7187

APPLICATION NUMBER: PCT/AU90/00530

FILING DATE: 02-NOV-1989

ATTORNEY/AGENT INFORMATION:

NAME: FEEDRATION NUMBER: 35,134

REGISTRATION NUMBER: 35,134
1424 ITITITITYKITGAAACCAATAATTTATCAAAA 1391
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           REFERENCE/DOCKET NUMBER: RICE-0002
TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-568-3439
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
BEDIUM TYPE: Floppy disk
CMBUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        5852 base pairs
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2378..5038
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Best Local Similarity
Matches 69; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRANDEDNESS:
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LOCATION:
FEATURE:
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FEATURE:
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STATE: PA
COUNTRY:
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; LOCATION:
US-07-867-106-2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    144 IGAAAGCAACGCTTGAAAAAAGGAAAGTTAGCCCTATCGGGTATATTTTGGAAGTTGTAA 203
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 89; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TILE OF INVENTION: 44 Human Secreted Proteins
FILE REFERENCE: P2024P1
CURRENT APPLICATION: 44 Human Secreted Proteins
FILE REFERENCE: P2024P1
CURRENT APPLICATION NUMBER: US/09/369,247
CURRENT FILING DATE: 1999-08-05
EARLIER FILING DATE: 1998-02-09
EARLIER APPLICATION NUMBER: 60/074,157
EARLIER APPLICATION NUMBER: 60/074,137
EARLIER APPLICATION NUMBER: 60/074,137
EARLIER FILING DATE: 1998-02-09
EARLIER FILING DATE: 1998-02-09
EARLIER FILING DATE: 1998-02-09
EARLIER FILING DATE: 1998-02-09
EARLIER FILING DATE: 1998-02-09
EARLIER FILING DATE: 1998-02-09
NUMBER OF SEQ. DID NOS: 172
SOFTWARE: PATENTIN OFF: 2.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 7.1%; Score 37.6; DB Best Local Similarity 50.6%; Pred. No. 15; Matches 91; Conservative 0; Mismatches
                                                                                       NAME/KEY: misc feature

LOCATION: (1602912)...(1602912)

OTHER INFORMATION: n equals a, t, c, or g

NAME/KEY: misc feature

LOCATION: (1603734)...(1603734)

OTHER INFORMATION: n equals a, t, c, or g

NAME/KEY: misc feature

LOCATION: (1637998)...(1637998)

OTHER INFORMATION: n equals a, t, c, or g

NAME/KEY: misc feature

LOCATION: (1664954)...(1664955)

US-08-916-421B-1
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Patent No. 6569992
GENERAL INFORMATION:
                    NAME/KEY: misc feature
LOCATION: (1569020)..(1569020)
OTHER INFORMATION: n equals a,
  OTHER INFORMATION: n equals a,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 60.6
Matches 57; Conservative
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US-09-369-247-23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     JS-09-369-247-23/c
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1540 AAAAA 1544
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-08-545-196B-12
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         45 GGTGATTTTGCTTCCTTTATACTTTATTTATTTCCCAAATTTTTCTTAAGCAAATAT 104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Gaps
                                                              GENERAL INFORMATION:
APPLICANT: MELKI, JUDITH
APPLICANT: MELKI, JUDITH
APPLICANT: MINNICH, ARNOLD
TITLE OF INVENTION: SURVIVAL MOTOR NEURON (SNN) GENE: A GENE
TITLE OF INVENTION: FOR SPINAL MUSCULAR ATROPHY
NUMBER OF SEQUENCES: 65
CORRESPONDENCE ADDRESS:
ADDRESSEE: BIRCH, STEWART, KOLASCH AND BIRCH, LLP
STREET: PO BOX 747
CTTY: PALLS CHURCH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 12, Application US/08545196B
Patent No. 6080577
GENERAL INFORMATION:
APPLICANT: MUNNICH, ARNOLD
TITLE OF INVENTION: SURVIVAL MOTOR NEURON (SMN) GENE: A GENE
TITLE OF INVENTION: FOR SPINAL MUSCULAR ATROPHY
NUMBER OF SEQUENCES: 65
CORRESPONDENCE ADDRESS:
ADDRESSEE: BIRCH, STEWART, KOLASCH AND BIRCH, LLP
STREET: PD BOX 747
CITY: FALLS CHURCH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              7.0%; Score 37; DB 3; Length 1582;
56.0%; Pred. No. 0.95;
tive 0; Mismatches 55; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                      CURRENT APPLICATION DATA:

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/545,196B
FILING DATE: 19-OCT-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:

NAME: FARACI, C. J.

REGISTRATION NUMBER: 2121-110P
TELECOMUNICATION INFORMATION:

TELECOMUNICATION INFORMATION:

TELECOMUNICATION INFORMATION:

TELEPRAM: (703) 205-8050
TELEPRAM: (703) 205-8050
TELEPRAM: (703) 205-8050
TELEPRAM: (703) 205-8050
TELEPRAM: (703) 205-8050
TELEPRAM: (703) 205-8050
US-08-545-196B-10; Sequence 10, Application US/08545196B; Patent No. 6080577
                                                                                                                                                                                                                                                                                                                       COUNTRY: USA
ZIP: 22040-0747
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE CHARACTERISTICS:
LENGTH: 1582 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Best Local Similarity 56.0
Matches 70; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  nucleic acid
EDNESS: double
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US-08-545-196B-12
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1420 Gricarigracientiriricrarcificiaraficitraaaagraraaaaaaaaaaararri 1479
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Fatent No. 6063610
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Silver, Gary W.
TITLE OF INVENTION: No. 6063610el Carboxylesterase Nucleic Acid
TITLE OF INVENTION: Molecules, Proteins and Uses Thereof
NUMBER OF SEQUENCES: 66
CORRESPONDENCE ADDRESS:
ADDRESSEE: Carol Talkington Verser, Ph.D.
STREET: 1225 Sharp Point Drive
CITY: Fort Collins
STREET: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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COUNTRY: USA
ZIP: 22040-0747
COMPUTER READABLE FORM:
MEDIUW TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/545,196B
FILLING DATE: 19-OCT-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: Windows 95
SOFTWARE: WordPerfect for Windows, Version 7.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     7.0%; Score 37; DB 3; 56.0%; Pred. No. 0.95; tive 0; Mismatches
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FILING DATE: No: 6063610ember 12, 1996
CLASSIFICATION: 45
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                             NAME: FARACI, C. J.
REGIGTRATION NUMBER: 32,350
REFERENCE/DOCKET NUMBER: 2121-110P
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 205-8000
TELEPAX: (703) 205-8050
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 1582 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CURRENT APPLICATION DATA:
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Matches 70; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: nucleic acid
STRANDEDNESS: doub
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COMPUTER REDABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: Windows 95
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INFORMATION FOR SEQ 1D NO: 36
SEQUENCE CHARACTERISTICS:
LENGTH: 2007 nucleotides
    STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          11..1594
                         TOPOLOGY: linear;
MOLECULE TYPE: CDNA
US-08-747-221B-38
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Best Local Similarity
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; LOCATION:
US-09-005-051-36
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   24 TGATTTATATGCTGATTTATGGGTGATTTTGCTTCCTTCTTTATACTTTTATTATTCCC 83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 38, Application US/08747221B
Patent No. 6063610
GENERAL INCORMATION:
APPLICANT: Silver, Gary W.
APPLICANT: Wisnewski, Nancy
TITLE OF INVENTION: No. 6063610el Carboxylesterase Nucleic Acid
TITLE OF INVENTION: Molecules, Proteins and Uses Thereof
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                                                                                                                                                                                                                                                                            Query Match 7.0%; Score 37; DB 3; Length 2007; Best Local Similarity 56.0%; Pred. No. 1.1;. Matches 70; Conservative 0; Mismatches 55; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: Windows 95
SOFTWARE: WordPerfect for Windows, Version 7.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/747,221B
FILING DATE: No. 606310ember 12, 1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADDRESSEE: Carol Talkington Verser, Ph.D. ADDRESSEE: Heska Corporation STREET: 1825 Sharp Point Drive CITY: Fort Collins STATE: Colorado COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ATTORNEY/AGENT INFORMATION:
NAME: Verser, Carol Talkington
REGISTRATION NUMBER: 37,459
Verser, Carol Talkington
             REGISTRATION NUMBER: 37,459
REFERENCE/DOCKET NUMBER: FC-1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 970/484-9505
INFORMATION FOR SEQ ID NO: 36:
SEQUENCE CHARACTERISTICS:
LENGTH: 2007 nucleotides
TYPE: nucleic acid
STRANDENDESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     REFERENCE/DOCKET NUMBER: FC
TELECOMMUNICATION INFORMATION:
TELEPHONE: 970/493-7272
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEFAX: 970/484-9505
INFORMATION FOR SEQ ID NO: 38:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LENGTH: 2007 nucleotides
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                        ) NAME/KEY: CDS
) LOCATION: 11..1594
US-08-747-221B-36
                                                                                                                                                                                                                                          TOPOLOGY: linear MOLECULE TYPE: CDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2003 AAAAA 2007
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 36, Application US/09005051
; Batent No. 6291222
; GENERAL INFORMATION:
    APPLICANT: Silver, Gary W.
    APPLICANT: Silver, Gary W.
    TITLE OF INVENTION: No. 6291222e1 Carboxylesterase Nucleic Acid
    TITLE OF INVENTION: No. 6291222e1 Carboxylesterase Nucleic Acid
    TITLE OF INVENTION: Molecules, Proteins and Uses Thereof
    NUMBER OF SEQUENCES: 66
    CORRESPONDENCE ADDRESS:
    ADDRESSEE: Heak Corporation
    STREET: 1825 Sharp Point Drive
    CITT: Port Collins
    STREET: USA
                                                                0; Gaps
Query Match 7.0%; Score 37; DB 3; Length 2007; Best Local Similarity 56.0%; Pred. No. 1.1; Matches 70; Conservative 0; Mismatches 55; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE: Worderfect for Windows, Version 7.0 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/005,051
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
PILING DATE:
NO. 6291222ember 12, 1996
ATYONREY/AGENT INFORMATION:
REGISTRATION NUMBER: 37,459
REFERENCE/DOCKET NUMBER: FC-1
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECHONE: 970/493-7272
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                                                                                                                                                                                    GENERAL INFORMATION:
APPLICANT: Artiushin, Sergey
APPLICANT: Stipkovits, Laslo
APPLICANT: Minion, F. Chris
TITLE OF INVENTION: PCR-Based Assay For Mycoplasma
TITLE OF INVENTION: Hyopneumoniae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATE:
APPLICATION NUMBER: US/08/062,632
FILING DATE: 18-MAY-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 37; DB Pred. No. 1.1; 0; Mismatches
                                                                                                                                                                                                                                                                                                             NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: Dickstein, Shapiro and Morin
STREET: 2101 L. St. NW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Thomas Jefferson University
APPLICANT: Raphael Rubin
APPLICANT: Manorama Tewari
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     148 AGCAACGCTTGAAAAAGGAA 168
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                                                                                                                                               Sequence 4, Application US/08062632
Patent No. 5712090
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 1, Application US/09234245
Patent No. 6509457
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ATTORNEY/AGENT INFORMATION:
NAME: Brady Jr., James W.
REGISTRATION NUMBER: 32,11:
REFERENCE/DOCKET NUMBER: 11:
TELECOMMUNICATION INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               7.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEPHONE: (202) 785-9700
TELEFAX: (202) 887-0689
INFORMATION FOR SEQ ID NO: 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE CHARACTERISTICS:
LENGTH: 2334 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 53.9
Matches 76; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             single
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MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE: 18-MAY CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                       SIRED...
CITY: Washington
STATE: D.C.
COUNTRY: USA
  144 TGAAA 148
                                           5 AAAAA 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                             22037
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US-09-234-245-1
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                                                                                                                                                                  1883 TTATTTATATTTGATATTATTACCATCTTTGTATCATATTTGCTTTTATTTTTTTCATTTT 1942
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                                           24 IGATITATATATGCTGATTTATGCTTTTTTCCTTCTTTTATACTTTTATTTCCC
  0; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
APPLICANT: Silver, Gary W.
APPLICANT: Silver, Gary W.
APPLICANT: Wisnewski, Nancy
TITLE OF INVENTION: No. 629122221 Carboxylesterase Nucleic Acid
TITLE OF INVENTION: Molecules, Proteins and Uses Thereof
NUMBER OF SEQUENCES: 66
CORRESPONDENCE ADDRESS:
ADDRESSEE: Carol Talkington Verser, Ph.D.
ADDRESSEE: Heska Corporation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0,
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55; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: Windows 95
SOFTWARE: Worderfect for Windows, Version 7.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/005,051
  Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/747,221
FILING DATE: No. 6291222ember 12, 1996
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STREET: 1825 Sharp Point Drive
CITY: Fort Collins
STATE: Colorado
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME: Verser, Carol Talkington REGISTRATION NUMBER: 37,459
                                                                                                                                                                                                                                                                                                                                                       Sequence 38, Application US/09005051
Patent No. 6291222
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REPERENCE/DOCKET NUMBER: FC
TELECOMMUNICATION
TELEPHONE: 970/493-7272
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEFAX: 970/484-9505
INFORMATION FOR SEQ ID NO: 38:
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  70; Conservative
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LENGTH: 2007 nucleotic
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
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US-09-005-051-38
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US-09-005-051-38/c
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  Matches
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Gaps

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92; Indels

Pred. No. 3.1; 0; Mismatches

50.04;

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40 THATGGGTGATTTTGCTTCCTTCTTTATACTTTTATTTCCCAAATTTTTCTTAAGCA
                          92; Conservative
  Best Local Similarity
Matches 92; Conserva
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                                                                                                                                                                                                                                                                                                  DB 4; Length 3715;
TITLE OF INVENTION: Compositions And Methods For Modulating TITLE OF INVENTION: Apoptosis FILE REFERENCE: TUU-002 CURRENT APPLICATION NUMBER: US/09/234,245 CURRENT APPLICATION NUMBER: US 60/071,878 EARLIER APPLICATION NUMBER: US 60/071,878 EARLIER FILING DATE: 1998-01-20 SOFTWARE: FAST OID NOS: 18 SOFTWARE: FAST OID NOS: 18 SOFTWARE: FAST OID NOS: 18
                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                            61 TCTTTATACTTTTATTTCCCAAATTTTTCTTAAGCAAATATTTC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
SOFTWARE: PAPLICATION DATA:
APPLICATION NUMBER: US/08/781,891
FILING DATE: 27-DEC-1996
                                                                                                                                                                                                                                                                                                                                      45;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             E: SEED and BERRY LLP
6300 Columbia Center, 701 Fifth Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILING DALE.

CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: No. 6090620tenburg Ph.D., Carol
REGISTRATION NUMBER: 39,317
REFERENCE/DOCKET NUMBER: 240052.419
TELECOMMUNICATION INFORMATION:
""".RPHONE: (206) 622-4900
                                                                                                                                                                                                                                                                                                                                      0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 208, Application US/08781891
Patent No. 6090620
GENERAL INFORMATION:
APPLICANT: Fu, Ying-Hui
APPLICANT: Fu, Chang-En
APPLICANT: Oshima, Junko
APPLICANT: Mulligan, John T.
APPLICANT: Schellenberg, Gerald D.
TITLE OF INVENTION: GENE AND GENE PRODUC
                                                                                                                                                                                                                                                                                                Score 37;
Pred. No. 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 208:
SEQUENCE CHARACTERISTICS:
LENGTH: 16442 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                              7.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           209
                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 58.7
Matches 64; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                       ; ORGANISM: Mus musculus
US-09-234-245-1
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Washington
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                                                                                                                                                                                                 LENGTH: 3715
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                                                                                                                                                                                                                         TYPE: DNA
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7.0%; Score 36.8; DB 3; Length 16442;

Query Match

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14571 CAAATTTCATTTTAGATTTTGAAAAGATTGTATAGGTTTAAACCTCTCAATTTCATTACA 14630
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160 AAAAAGGAAAGTTAGCCCTATCGGGTATATTTTGGAAGTTGTAAAATACTACRTGTTCTC 219
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Fu, Ying-Hui
Yu, Chang-En
Oshima, Junko
Mulligan, John T.
Schellenberg, Gerald D.
TITLE OF INVENTION: GENE AND GENE PRODUCTS RELATED TO
WERNER'S SYNDROME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CORRESPONDENCE ADDRESS:
ADDRESSE: Seed Intellectual Property Law Group STREET: 701 Fifth Avenue, Suite 6300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMEATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/618,166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME: MCMABLETB, DAVIG D.
REGISTRATION NUMBER: 33,963
REFERENCE/DOCKET NUMBER: 240052.419C1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
TELEFRAX: (206) 682-6031
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TOPOLOGY: linear ; SEQUENCE DESCRIPTION: SEQ ID NO: 208: US-09-618-166-208
                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 208, Application US/09618166
Patent No. 6583112
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE: 17-Jul-2000
CLASSIFICATION: <UNKNOWN>
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LENGTH: 16442 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              INFORMATION FOR SEQ ID NO: 206
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQUENCES: 209
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CITY: Seattle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COUNTRY: USA
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Best Local Similarity
                                                                                                                                                                                                                                                                                            14691 TTGT 14694
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Matches 65; Conserv
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US-09-453-323-1
                                                                                                                                                                                                                             TYPE: DNA
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                                   14571 CAAATTTCATTTTAGATTTTGAAAAGATTGTATAGGTTTAAACCTCTCAATTTCATTACA 14630
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160 AAAAAGGAAAGTTAGCCCTATCGGGTATATTTTGGAAGTTGTAAAATACTACRTGTTCTC 219
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                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
APPLICANT: Rosen et al
TITLE OF INVENTION: 98 Human Secreted Proteins
                                                                                                                                                                                                                                                                                                                                                                      TILE REFERENCE: PEO31PI
CURRENT APPLICATION NUMBER: US/09/489,847
CURRENT FILING DATE: 2000-01-24
EARLIER APPLICATION NUMBER: PCT/US99/17130
EARLIER APPLICATION NUMBER: PCT/US99/17130
EARLIER APPLICATION NUMBER: 60/094,657
EARLIER APPLICATION NUMBER: 60/094,657
EARLIER APPLICATION NUMBER: 60/095,486
EARLIER FILING DATE: 1998-08-05
EARLIER FILING DATE: 1998-08-05
EARLIER FILING DATE: 1998-08-10
EARLIER FILING DATE: 1998-08-10
EARLIER FILING DATE: 1998-08-06
EARLIER FILING DATE: 1998-08-06
EARLIER FILING DATE: 1998-08-06
SEARLIER FILING DATE: 1998-08-06
SEARLIER FILING DATE: 1998-08-06
SEARLIER FILING DATE: 1998-08-06
SOFTWARE: PALEND NOS: 376
SOFTWARE: PALEND NOS: 376
SEQID NO 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; LOCATION: (951)
; OTHER INFORMATION: n equals a,t,g, or
US-09-489-847-112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
                                                                                                                                                                                                                                                                                Sequence 112, Application US/09489847 Patent No. 6476195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LOCATION: (936)
OTHER INFORMATION: n equals a,t,g,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 37
US-08-894-731-2
Sequence 2, Application US/08894731
Fatent No. 6084089
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME/KEY: SITE
LOCATION: (946)
OTHER INFORMATION: n equals
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                    14691 TṛGT 14694
                                                                                                                                                  220 TTCT 223
                                                                                                                                                                                                                                            RESULT 36
US-09-489-847-112/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FEATURE:
NAME/KEY: SITE
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US-09-328-352-642

Sequence 642, Application US/09328352

Sequence 642, Application US/09328352

Sequence 642, Application US/09328352

Sequence 642, Application US/09328352

GENERAL INFORMATION:

APPLICANT: Gary L. Breton et al.

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER

TITLE OF INVENTION: BAUMANNII FOR DIAGNOSTICS AND THERAPEUTICS

FILE REPERENCE: GTC99-0378

CURRENT APPLICATION NUMBER: US/09/328,352

CURRENT PILING DATE: 1999-06-04

NUMBER OF SEQ ID NOS: 8252

SEQ ID NO 642
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TITATACTITITATITATICCCAAAITITICITAAGCAAATATITCTITGCTAATCAATAA 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  61 Triritagcactraaaatarriraaaaagrggraactraarraaraaaacaaaaagaaargag 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 1, Application US/09453323
Patent No. 6441272
GENERAL INFORMATION:
A APPLICANT: Ye, Zheng-Hua
TITLE OF INVENTION:
TITLE OF INVENTION:
TITLE OF INVENTION:
FILE REFERENCE: 235.00090101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      6.8%; Score 36.2; DB 4; Length 318; larity 57.5%; Pred. No. 0.77; Conservative 0; Mismatches 48; Indels
APPLICANT: OHYAMA, AKIO.
APPLICANT: HIYOSHI, Toru.
APPLICANT: HIYOSHI, Toru.
APPLICANT: KASAOKA, Keisuke,
ITILE OF INVENTION: COLD-INDUCIBLE PROMOTER SEQUENCE;
ITILE REFERENCE: 760-234P;
CURRENT BILING DATE: 1997-10-27;
NUMBER OF SEQ ID NOS: 8
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 2
LENGTH: 4140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              123 ATTATCAAAGAAAAAAAACT 144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      346 ATCAATATAGATAATTAAATCT 367
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ORGANISM: Acinetobacter baumannii US-09-328-352-642
                                                                                                                                                                                                                                                                                                                                                                    ; ORGANISM: Solanum tuberosum
US-08-894-731-2
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APPLICANT: Pallas, David C
APPLICANT: Pallas, David C
APPLICANT: Du, Xianxing
TITLE OF INVENTION: Coding Sequence for Protein Phosphatase Methylesterase,
TITLE OF INVENTION: Recombinant DNA Molecules and Methods
FILE REFERENCE: 105-97
CURRENT FILING DATE: 1999-04-16
FRIOR TILING DATE: 1999-04-17
FRIOR FILING DATE: 1999-04-17
NUMBER: OF SEQ ID NOS: 17
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 8
FENDING TILING DATE: 2009-04-17
NUMBER: PatentIn Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PAPLICANT: Du, Xianning
TITLE OF INVENTION: Coding Sequence for Protein Phosphatase Methylesterase,
Parent No. 6528295
TITLE OF INVENTION: Recombinant DNA Molecules and Methods
TITLE OF INVENTION: Recombinant DNA Molecules and Methods
TITLE OF INVENTION: Recombinant DNA Molecules and Methods
TITLE REPERBUCE: Docket No. 6528295 105-97A
CURRENT APPLICATION NUMBER: US/09/839,497A
CURRENT FILING DATE: 1988-60/082,202
PRIOR APPLICATION NUMBER: 60/082,202
PRIOR APPLICATION NUMBER: 09/293,322
PRIOR PILING DATE: 1989-04-16
NUMBER OF SEQ ID NOS: 17
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 8
SEQ ID NO 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2300 ictitgitatitatgarciigittaaagaaaataaatarciccaaccittaaaaaaaa 2359
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             70 TITTATITIATICCCAAATITITICTITAAGCAAATATITICTITIGCTAATCAATAAATTATCA 129
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Pred. No. 2.2;
0; Mismatches 40; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             40; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     130 AAAGAAAAAAAACTGAAAGCAACGCTTGAAAAAAGGAAA 169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; Score 36; DB 4
; Pred. No. 2.2;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME/KEY: misc_feature

LOCATION: (1)..(2409)

OTHER INFORMATION: N is A, T, G or C.

US-09-293-122C-8
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: LOCATION: (1)..(2409)

: OTHER INFORMATION: N is A, T, G or C.

US-09-839-497A-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 8, Application US/09839497A
Patent No. 6528295
GENERAL INFORMATION:
APPLICANT: Pallas, David C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 60.0%;
Matches 60; Conservative
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Best Local Similarity 60.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: DNA ORGANISM: Mus musculus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 82 CCAAATTTTTCTTAAGCAAATATTTCTTTGCTAATCAATAAATTATCAAAAGAAAAAAA 141
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                                                                                                                                                                                                                                                                                                                                                                                                   46 GIGATITIGCTICCTITATACTITITATICCCAAATTITICTIAAGCAAATATT
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                                                                                                                                                                                                                                                                                                  DB 4; Length 1507;
                                                                                                                                                                                                                                                                                                                                                     55; Indels
                                                                                                                                                                                                                                                                                                ch 6.8%; Score 36; DB 4
1 Similarity 55.6%; Pred. No. 1.8;
69; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 59, Application US/08821994A
| Patent No. 6228643
| GENERAL INFORMATION:
| APPLICANT: Greenland, Andrew J
| APPLICANT: Greenland, Andrew J
| APPLICANT: Greenland, Ean
| APPLICANT: Thomas, Didier RP
| APPLICANT: Thomas, Didier RP
| TILE OF INVENTION: Promoters
| FILE REFERENCE: PPD 50108
| CURRENT APPLICATION WUMBER: US/08/821,994A
| CURRENT FILING DATE: 1997-03-18
| EARLIER FILING DATE: 1997-03-18
| EARLIER FILING DATE: 1996-03-22
| MUMBER OF SEQ ID NOS: 89
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CURRENT APPLICATION NUMBER: US/09/453,323
CURRENT FILING DATE: 1999-12-02
PRIOR PILING DATE: 1998-12-02
NUMBER OF SEQ ID NOS: 13
SOFTWARE: PatentIn Ver. 2.0
LENGTH: 1507
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                                                                                                                                                                                                 TYPE: DNA ORGANISM: Nicotiana tabacum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 59
LENGTH: 1577
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; TYPE: DNA
; ORGANISM: Brassica napus
US-08-821-994-59
                                                                                                                                                                                                                                                                                                                            Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1477 AAAA 1480
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US-09-293-322C-8
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US-08-821-994-59
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LOCATION:
US-08-738-349-1
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Best Local S
Matches 78
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APPLICANT: Cassell, Gail H.
APPLICANT: Cassell, Gail H.
APPLICANT: Cassell, Gail H.
APPLICANT: Glass, Jennifer S.
APPLICANT: Glass, John I.
APPLICANT: Heiner, Cherryl R.
APPLICANT: Heiner, Cherryl R.
APPLICANT: Lefkowitz, Elliot
ITILE OF INVENTION: UNEALYITCUM
ITILE OF INVENTION: UNEALYITCUM
ITILE OF INVENTION: UNEALYITCUM
ITILE OF INVENTION: UNBERS: 2000-12-08
ITILE REPERENCE: 2000-12-08
ICURRENT FILING DATE: 2000-12-08
IPRIOR PLICATION NUMBER: 60/073,189
IPRIOR FILING DATE: 1998-01-30
INVENTE OF TOWNER: 1198-01-30
INVENTE OF TOWNER: PATENTIN VEY: 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2218 ATTCTGCATTAGCTAAAACTTTAAACGATÄTTTAATTTTTAGTTTCTTAATTAATAAAT 2159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2158 TGTTTTGATCATATTCAAGTTCTTTACTTGTGATTTCAGGCTTGCTAATCCCATATTTAA 2099
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2098 AATATGATTTTAAATCATTAATTGAAGGATCATTAGATGTAATTTTTGGATATAAAATAG 2039
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    68 ACTITITATITCCCAAATTITICTIAAGCAAATATITCTITGCTAATCAATAATTAT 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       128 CAAAAGAAAAAAAACTGAAAGCAACGCTTGAAAAAAGGAAAGTTAGCCCTATCGGGTAT 187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    8 ATGCTGTAGTCGTGGCTGATTTATATGTGTTTATGGGTGATTTTGCTTCTTTAT 67
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APPLICANT: Okazaki, Makoto
APPLICANT: Kawai, Shinji
APPLICANT: Taujimura, Ataushi
APPLICANT: Taujimura, Ataushi
APPLICANT: Amani, Egon
TITLE OF INVENTION: Bone-Related Cadherin-Like Protein and
TITLE OF INVENTION: Process for Its Production
CORRESPONDENCE: 12
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 6.8%; Score 36; DB 4; Length 3165; Best Local Similarity 47.7%; Pred. No. 2.5; Matches 105; Conservative 0; Mismatches 115; Indels
                                              2038 CAİCTAAAAGİTTITTAATATİTTCİTTATITCAATTAĞİ 1999
130 AAAGAAAAAAAACTGAAAGCAACGCTTGAAAAAGGAAA 169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        188 ATTITGGAAGTIGTAAAATACTACRIGTICTCTTTAAGT 227
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADDRESSEE: Finnegan, Henderson, Farabow, Garrett & ADDRESSEE: Dunner
                                                                                                                                                                         Sequence 102, Application US/09601198
Patent No. 6531583
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; Sequence 1, Application US/08738349; Patent No. 5869638; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: DNA ORGANISM: Ureaplasma urealyticum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STREET: 1300 I Street, N.W.
CITY: Washington
STATE: D.C.
                                                                                                                       RESULT 43
US-09-601-198-102/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQ ID NO 102
LENGTH: 3165
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73 TATTTATTCCCAAATTTTTCTTAAGCAAATATTTCTTTGCTAATCAATAAATTATCAAAA 132
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            13 GTAGTCGTGGCTGATTTATATGCTGATTTATGGGTGATTTTGCTTCCTT
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/738,349
FILING DATE: 25-OCT-1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION: WINBER: US/08/364,439
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Fischer et al.
TITLE OF WINVENTION: 123 Human Secreted Proteins
FILE REFERENCE: PZO10P1
CURRENT APPLICATION NUMBER: US/09/227,357
CURRENT APPLICATION NUMBER: US/09/227,357
CURRENT APPLICATION NUMBER: OF/US98/13684
EARLIER APPLICATION NUMBER: PCT/US98/13684
EARLIER APPLICATION NUMBER: 06/051,926
EARLIER FILING DATE: 1997-07-08
EARLIER APPLICATION NUMBER: 60/052,793
EARLIER APPLICATION NUMBER: 60/051,925
EARLIER FILING DATE: 1997-07-08
EARLIER FILING DATE: 1997-07-08
EARLIER FILING DATE: 1997-07-08
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EARLIER FILING DATE: 1997-07-08
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RRR: 02481.1323-00000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           133 GAAAAAAAACTGAAAGCAACGCTTGAA 160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN: osteoblastic cell line MC3T3E1
                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: US 08/112,061
FILING DATE: 26-AUG-1993
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-09-227-357-76/c
; Sequence 76, Application US/09227357
; Patent No. 6342581
                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME: Barker, M. P.
REGISTRATION NUMBER: 32,013
REPERENCE/DOCKET NUMBER: 024(
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-408-4000
TELEFAX: 202-408-4400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 3581 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MOLECULE TYPE: CDNA to mRNA ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CDS
284..2671
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EARLIER APPLICATION NUMBER: 60/058,785
EARLIER FILING DATE: 1997-09-12
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EARLIER FILING DATE: 1997-09-12
EARLIER PILING DATE: 1997-09-12
EARLIER FILING DATE: 1997-09-12
EARLIER FILING DATE: 1997-09-12
NUMBER OF SEQ ID NOS: 672
SOFTWARE: Patentin Ver. 2.0
                                                            R PILING DATE: 1997-07-08

R APPLICATION NUMBER: 60/051,931

R PILING DATE: 1997-07-08

R PILING DATE: 1997-07-08

R PILING DATE: 1997-07-08

R APPLICATION NUMBER: 60/051,932
                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: 60/052,733
FILING DATE: 1997-07-08
APPLICATION NUMBER: 60/052,795
FILING DATE: 1997-07-08
APPLICATION NUMBER: 60/051,919
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PEATURE:
NAME/KEY: SITE
LOCATION: (24)
OTHER INFORMATION: n equals a,t,g, or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE: 1997-08-18
APPLICATION NUMBER: 60/055,948
FILING DATE: 1997-08-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ILING DATE: 1997-08-18
PRICATION NUMBER: 60/055,953
PRING DATE: 1997-08-18
PRIICATION NUMBER: 60/055,950
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE: 1997-07-08
APPLICATION NUMBER: 60/051,928
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: 60/055,949
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE: 1997-08-18
APPLICATION NUMBER: 60/055,947
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TLING DATE: 1997-08-18
PPLICATION NUMBER: 60/056,360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE: 1997-08-18
APPLICATION NUMBER: 60/055,684
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EARLIER APPLICATION NUMBER: 60/055,954
EARLIER FILING DATE: 1997-08-18
PLICATION NUMBER: 60/052,803
LING DATE: 1997-07-08
                                             LICATION NUMBER: 60/052,732
                                                                                                                                                                                                                                                                   APPLICATION NUMBER: 60/051,918
                                                                                                                                                                                                                                                                                                                      PPLICATION NUMBER: 60/051,920
ILING DATE: 1997-07-08
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE: 1997-07-08
APPLICATION NUMBER: 60/055,722
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE: 1997-08-18
APPLICATION NUMBER: 60/055,723
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE: 1997-08-18
APPLICATION NUMBER: 60/055,964
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EARLIER FILING DATE: 1997-08-18
EARLIER APPLICATION NUMBER: 60/055,984
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FEATURE:
NAME/KEY: SITE
LOCATION: (13)
OTHER INFORMATION: n equals a,t,g,
                                                                                                                                                                                                                                                                                                  LING DATE: 1997-07-08
                                                                                                                                                                                                            FILING DATE: 1997-07-08
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQ ID NO 76
LENGTH: 519
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CONTION: (35)

CONTENT INCORMATION: n equals a,t,g, or c

ERATURE:
ERATURE:
ELACATION: (44)

CONTENT INFORMATION: n equals a,t,g, or c

US-09-227-357-76

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